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QM nucleic - nucleic search, using sw model

Run on: April 27, 2005, 17:25:16 ; Search time 1427 Seconds
(without alignments)
10835.997 Million cell updates/sec

Title: US-09-989-739-18
Perfect score: 2547
Sequence: 1 ccattggtcgatcttcccc.....gctggtggtgctgtcgtt 2547

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5633728 seqs, 3035525691 residues

Total number of hits satisfying chosen parameters: 11267456

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2547	100.0	2547	10	US-09-989-739-18
2	399	15.7	2291	18	US-10-425-115-86750
3	203	8.0	957	17	US-10-425-114-1414
c	181	7.1	289	18	US-10-425-115-32558
5	132	5.2	1044	18	US-10-425-115-141079
6	132	5.2	1316	17	US-10-425-114-22834
7	132	5.2	1342	18	US-10-425-115-141080
8	132	5.2	1359	17	US-10-425-114-19533
9	132	5.2	1413	17	US-10-425-114-17319
10	132	5.2	1426	17	US-10-425-114-773
11	132	5.2	1605	17	US-10-425-114-32327

12	132	5.2	1638	18	US-10-425-115-141081	Sequence 141081,
13	132	5.2	1800	18	US-10-425-115-141084	Sequence 141084,
14	122.4	4.8	706	18	US-10-767-701-12658	Sequence 12658, A
15	108	4.2	860	18	US-10-425-115-165740	Sequence 165740,
16	107.2	4.2	3001	16	US-10-338-777-4	Sequence 4, Appli
17	104.8	4.1	1093	17	US-10-425-114-36130	Sequence 36130, A
18	104.8	4.1	1353	17	US-10-425-114-30712	Sequence 30712, A
19	104.8	4.1	1431	17	US-10-425-114-35310	Sequence 35310, A
20	104.8	4.1	1440	17	US-10-425-114-1405	Sequence 1405, Ap
21	104.8	4.1	1463	17	US-10-425-114-22195	Sequence 22195, A
22	104.8	4.1	1622	18	US-10-425-115-10088	Sequence 10088, A
23	104.8	4.1	1623	18	US-10-425-115-67912	Sequence 67912, A
24	104	4.1	1524	18	US-10-739-930-2495	Sequence 2495, Ap
25	103.2	4.1	1326	17	US-10-425-114-14399	Sequence 14399, A
26	103.2	4.1	1376	18	US-10-425-115-110179	Sequence 110179,
27	103.2	4.1	1431	18	US-10-425-115-109303	Sequence 109303,
28	103.2	4.1	1456	17	US-10-425-114-27579	Sequence 27579, A
29	103.2	4.1	1490	18	US-10-739-930-2497	Sequence 2497, Ap
30	103.2	4.1	1503	17	US-10-425-114-22084	Sequence 22084, A
31	103.2	4.1	1508	17	US-10-425-114-21570	Sequence 21570, A
32	103.2	4.1	1561	18	US-10-425-115-67911	Sequence 67911, A
33	103.2	4.1	1568	18	US-10-437-963-28028	Sequence 28028, A
34	103.2	4.1	1570	18	US-10-425-115-109304	Sequence 109304,
35	103.2	4.1	2078	18	US-10-425-115-108405	Sequence 108405,
36	102.2	4.0	1392	17	US-10-425-114-21120	Sequence 21120, A
37	102.2	4.0	2438	18	US-10-425-115-67915	Sequence 67915, A
38	101.4	4.0	1348	17	US-10-425-114-30956	Sequence 30956, A
39	101.4	4.0	1348	18	US-10-425-115-67904	Sequence 67904, A
40	101	4.0	281	9	US-09-923-876-4439	Sequence 4439, Ap
41	101	4.0	281	10	US-09-923-876-4439	Sequence 4439, Ap
42	100.6	3.9	1352	17	US-10-425-114-21011	Sequence 21011, A
43	100.6	3.9	1552	17	US-10-425-115-10090	Sequence 10090, A
44	98.6	3.9	693	17	US-10-260-238-5656	Sequence 5656, Ap
c	98.4	3.9	1915	18	US-10-767-701-15746	Sequence 15746, A

ALIGNMENTS

= instant cage

RESULT 1
US-09-989-739-18
; Sequence 18, Application US/09989739
; Publication No. US20030140364A1
; GENERAL INFORMATION:
; APPLICANT: HINCHEY, BRENDAN
; APPLICANT: SONG, HEE-SOOK
; TITLE OF INVENTION: MAIZE CYTOPLASMIC GLUTAMINE SYNTHETASE PROMOTER
; FILE REFERENCE: DEKM:177US
; CURRENT APPLICATION NUMBER: US/09/989,739
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 2547
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-989-739-18

Query Match	100.0%	Score 2547;	DB 10;	Length 2547;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2547;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	CCATGGTCCGTACCTTCCCTCGCTGCACAAATGAACCGACCTGTTGCGTACAGACATT	60	
Db	1	CCATGGTCCGTACCTTCCCTCGCTGCACAAATGAACCGACCTGTTGCGTACAGACATT	60	
QY	61	TCGTGGAATGGTCTTCTTACGCTGAGCCTGTGTAATCCAGGTTCCGGATTGAGCAGG	120	
Db	61	TCGTGGAATGGTCTTCTTACGCTGAGCCTGTGTAATCCAGGTTCCGGATTGAGCAGG	120	

Db 2281 AATATATTAATAGATAGATATATTTCTCACCACAAATCACTACAGTACAACTTTACG 2340
Qy 2341 AGTGACCCGGATGAGTCGAGGAGACAAACGTTACACGCGCCCTTGAGAACACTTTCC 2400
Db 2341 AGTGACCCGGATGAGTCGAGGAGACAAACGTTACACGCGCCCTTGAGAACACTTTCC 2400
Qy 2401 AAGCCAGAGGACCTACACCAACCACTCTCGGGCTCTGCTCTATTATTATGAGGAGCAGCC 2460
Db 2401 AAGCCAGAGGACCTACACCAACCACTCTCGGGCTCTGCTCTATTATTATGAGGAGCAGCC 2460
Qy 2461 AGCTACAGGCTACAGCCTGCGGAAAGACACACGAGTCAATCACTCATCTCGGGGCA 2520
Db 2461 AGCTACAGGCTACAGCCTGCGGAAAGACACACGAGTCAATCACTCATCTCGGGGCA 2520
Qy 2521 TTGTCCTGCTCGTGGCTCTCTGCTT 2547
Db 2521 TTGTCCTGCTCGTGGCTCTCTGCTT 2547

RESULT 2
US-10-425-115-86750
; Sequence 86750, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 86750
; LENGTH: 2291
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_179122C.1
US-10-425-115-86750

Query Match 15.7%; Score 399; DB 18; Length 2291;
Best Local Similarity 100.0%; Pred. No. 2e-73;
Matches 399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCATGGTCCGTACCTTCCCTCGCTGACGAAATGAACCGACCTGTTGCGTACAGACATT 60
Db 526 CCATGGTCCGTACCTTCCCTCGCTGACGAAATGAACCGACCTGTTGCGTACAGACATT 585
Qy 61 TCGTCGAAATGGTCTTCTTACGCTGAGCCTGTGTAATCCAGTTGCGGATTGAGCAGG 120
Db 586 TCGTCGAAATGGTCTTCTTACGCTGAGCCTGTGTAATCCAGTTGCGGATTGAGCAGG 645
Qy 121 AGTACACCTTCTCCAGAGGACACCAAGTGGCCCTCTCGGTTGGCGCTGCGGCGCTACC 180
Db 646 AGTACACCTTCTCCAGAGGACACCAAGTGGCCCTCTCGGTTGGCGCTGCGGCGCTACC 705
Qy 181 CTGGCCCTCAGGTAGATTAGATTCGCTGCTCCAGGCTCCAGGCTATCGATGGC 240
Db 706 CTGGCCCTCAGGTAGATTAGATTCGCTGCTCCAGGCTCCAGGCTATCGATGGC 765
Qy 241 TTTGATCAGCTGACGGAATGATCTCGGAGGACCTTACTACTCGCGCTCGGAGCGGAC 300
Db 766 TTTGATCAGCTGACGGAATGATCTCGGAGGACCTTACTACTCGCGCTCGGAGCGGAC 825
Qy 301 AAGTCCTACGGCGGGACATCGTGACGCGCACTACAGGCTGCTCTACGCGGCAATC 360
Db 826 AAGTCCTACGGCGGGACATCGTGACGCGCACTACAGGCTGCTCTACGCGGCAATC 885
Qy 361 GACATCAGTGATCAACCGGAGGATCATCGCGGGCAG 399

Db 886 GACATCAGTGGCATCAACGGGGAGGTCTATGCCGGGCGAC 924
RESULT 3
US-10-425-114-1414
; Sequence 1414, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 1414
; LENGTH: 957
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700152411_FLI
US-10-425-114-1414

Query Match 8.0%; Score 203; DB 17; Length 957;
Best Local Similarity 78.7%; Pred. No. 2.2e-32;
Matches 292; Conservative 0; Mismatches 0; Indels 79; Gaps 1;
Qy 29 CGAAATGAACCGACCTGTTGCGTACAGACATTTCTCGTGAATGTTCTTTACGCTGAG 88
Db 1 CGAAATGAACCGACCTGTTGCGTACAGACATTTCTCGTGAATGTTCTTTACGCTGAG 60
Qy 89 CCTGTGTAATCCAGTTGCGGATTGAGCAGGAGTACACCCCTTCTCCAGAGGACACCAA 148
Db 61 CCTGTGTAATCCAGTTGCGGATTGAGCAGGAGTACACCCCTTCTCCAGAGGACACCAA 120
Qy 149 GTGGCCTCTCGTTGGCGCTGGCGGCTACCCCTGGCCCTCAGGTAGATTAGATGATCT 208
Db 121 GTGGCCTCTCGTTGGCGCTGGCGGCTACCCCTGGCCCTCAGGTAGATTAGATGATCT 160
Qy 209 GCGTGCCTCCAGGCTCCAGCCATATCGATGCTTTGATCAGCTGACGGAATGATCTCGC 268
Db 161 -----C 161
Qy 269 AGGACCTTACTACTGCGCGCTCGGAGCGGACAAAGTCTACGGGCGGACATCGTGGACG 328
Db 162 AGGACCTTACTACTGCGCGCTCGGAGCGGACAAAGTCTACGGGCGGACATCGTGGACG 221
Qy 329 CGCACTACAGGCTGCTCTACGCGGCTACGATCGATCGATCGATCGATCGATCGATCGA 388
Db 222 CGCACTACAGGCTGCTCTACGCGGCTACGATCGATCGATCGATCGATCGATCGATCGA 281
Qy 389 TGCCGGGGCAG 399
Db 282 TGCCGGGGCAG 292

RESULT 4
US-10-425-115-32558/c
; Sequence 32558, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B

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; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 32558
; LENGTH: 289
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_129
US-10-425-115-32558

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Query Match	7.1%;	Score 181;	DB 18;	Length 289;
Best Local Similarity	85.8%;	Pred. No. 5.3e-28;		
Matches 248;	Conservative 0;	Mismatches 35;	Indels 6;	Gaps 4;
Qy	241	TTTGATCAGCTGACGGAATGATCTCGCAGGGACCTTACTACTCGCGCTCGGA--GCGG	298	
Db	289	TTTGATCAGCTGACGCAATGATAGTGCAGGGACCTTCATACTSCGCGTCGGACCGGA	230	
Qy	299	ACAAGTCTACGGCGGGACATCGTGACGGGCATCAAGGCTGCTCTACGCGGCA	358	
Db	229	CAGCTCCTACGGCGGGACATCGTGACGGGCATCAAGGCTGCTCTACGCGGCA	170	
Qy	359	TCGACATCA--GTGSCATCAACGGGGAGGTGATGCGGGGCGAGGTACAGCGTGTGCTCTA	417	
Db	169	TCGACATCAATGSCATCATCGGTGAGGTGATACCGGGCGAGGTACAGCGTGTGCTCTA	110	
Qy	418	GCTACCTTGCTTTAACTGCACACTGCACCTGCACACTGCACAGCTAGT--AGTATGCTG	476	
Db	109	GTCCTCTTGCTTTCCCTTGCAACCGGCATTTTGACACTGCTCAGCTAGTCAGTATGCTG	50	
Qy	477	CTATCTCTGCTGACCCA--GGCTTGTTCGTGGACAGTGGGAGTTCCAGG	523	
Db	49	CCATCTCTGCTCACTACGGCTTGCTCAGGGTTTCAGTCGGAGTTCAGG	1	

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RESULT 5
US-10-425-115-141079
; Sequence 141079, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 141079
; LENGTH: 1044
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_60146C.1
US-10-425-115-141079

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	Query Match	5.2%;	Score 132;	DB 18;	Length 1044;
	Best Local Similarity	100.0%;	Pred. No. 2e-17;		
	Matches 132;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	268	CAGGGA	CCTTACTACTCGCGCTCGGAGCGGACAAGTCTCTACGGCGGGGACATCGTGGAC	327	
Db	307	CAGGGA	CCTTACTACTCGCGCTCGGAGCGGACAAGTCTCTACGGCGGGGACATCGTGGAC	366	
Qy	328	CGGCAC	TACAAGGGCTCGCTCTACGCCGGGCATCGACATCAAGTGGCATCAACACGGGGAGTGC	387	
Db	367	CGGCAC	TACAAGGGCTCGCTCTACGCCGGGCATCGACATCAAGTGGCATCAACACGGGGAGTGC	426	
Qy	388	ATGCCGGGGCAG		399	

Db 427 ATGCCGGGCAG 438

RESULT 6

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US-10-425-114-22834
; Sequence 22834, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 22834
; LENGTH: 1316
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3591-121-H10_FLI
US-10-425-114-22834

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	Query Match	5.2%	Score 132;	DB 17;	Length 1316;
	Best Local Similarity	100.0%;	Pred. No. 2.3e-17;		
	Matches 132;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	268	CAGGGACCTTACTACTGCGCGCTCGGAGCGGACAAGTCTTACGGGCGGGACATCGTGGAC	327		
Db	514	CAGGGACCTTACTACTGCGCGCTCGGAGCGGACAAGTCTTACGGGCGGGACATCGTGGAC	573		
QY	328	GCGCACTACAAGGCGCTGCCTTACGCGCGGCATCGACATCAGTGGGCATCAACGGGGAGGTC	387		
Db	574	GCGCACTACAAGGCGCTGCCTTACGCGCGGCATCGACATCAGTGGGCATCAACGGGGAGGTC	633		
QY	388	ATGCCGGGGGAG	399		
Db	634	ATGCCGGGGGAG	645		

RESULT 7

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US-10-425-115-141080
; Sequence 141080, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425.115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 141080
; LENGTH: 1342
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577_60147C.1
US-10-425-115-141080

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Query Match 5.2%; Score 132; DB 18; Length 1342;
 Best Local Similarity 100.0%; Pred. No. 2.3e-17;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 268 CAGGGACCTTACTACTCGCGCGGAGCGGACAAAGTCCTTACGGGGCGGACATCGTGAC 327

```

Db      514 CAGGACCTTACTACTGCGCGTCCGAGCGGACAAAGTCTTACGGCGGGACATCGTGGAC 573
Qy      328 GCGCACTACAAGCCTGCTTACGCCGCGCATCGACATCAGTGGCATCAACGGGGAGGTC 387
Db      574 GCGCACTACAAGCCTGCTTACGCCGCGCATCGACATCAGTGGCATCAACGGGGAGGTC 633
Qy      388 ATGCCGGGGCAG 399
Db      634 ATGCCGGGGCAG 645

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RESULT 8

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US-10-425-114-19533
; Sequence 19533, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 19533
; LENGTH: 1359
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3150-045-F7_FLI
US-10-425-114-19533

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Query Match      5.2%; Score 132; DB 17; Length 1359;
Best Local Similarity 100.0%; Pred. No. 2.3e-17;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      268 CAGGACCTTACTACTGCGCGTCCGAGCGGACAAAGTCTTACGGCGGGACATCGTGGAC 327
Db      563 CAGGACCTTACTACTGCGCGTCCGAGCGGACAAAGTCTTACGGCGGGACATCGTGGAC 622
Qy      328 GCGCACTACAAGCCTGCTTACGCCGCGCATCGACATCAGTGGCATCAACGGGGAGGTC 387
Db      623 GCGCACTACAAGCCTGCTTACGCCGCGCATCGACATCAGTGGCATCAACGGGGAGGTC 682
Qy      388 ATGCCGGGGCAG 399
Db      683 ATGCCGGGGCAG 694

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RESULT 9

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US-10-425-114-17319
; Sequence 17319, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 17319
; LENGTH: 1413

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; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3069-006-G11_FLI
US-10-425-114-17319

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Query Match      5.2%; Score 132; DB 17; Length 1413;
Best Local Similarity 100.0%; Pred. No. 2.4e-17;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      268 CAGGACCTTACTACTGCGCGTCCGAGCGGACAAAGTCTTACGGCGGGACATCGTGGAC 327
Db      454 CAGGACCTTACTACTGCGCGTCCGAGCGGACAAAGTCTTACGGCGGGACATCGTGGAC 513
Qy      328 GCGCACTACAAGCCTGCTTACGCCGCGCATCGACATCAGTGGCATCAACGGGGAGGTC 387
Db      514 GCGCACTACAAGCCTGCTTACGCCGCGCATCGACATCAGTGGCATCAACGGGGAGGTC 573
Qy      388 ATGCCGGGGCAG 399
Db      574 ATGCCGGGGCAG 585

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RESULT 10

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US-10-425-114-773
; Sequence 773, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 773
; LENGTH: 1426
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700092738_FLI
US-10-425-114-773

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Query Match      5.2%; Score 132; DB 17; Length 1426;
Best Local Similarity 100.0%; Pred. No. 2.4e-17;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      268 CAGGACCTTACTACTGCGCGTCCGAGCGGACAAAGTCTTACGGCGGGACATCGTGGAC 327
Db      541 CAGGACCTTACTACTGCGCGTCCGAGCGGACAAAGTCTTACGGCGGGACATCGTGGAC 600
Qy      328 GCGCACTACAAGCCTGCTTACGCCGCGCATCGACATCAGTGGCATCAACGGGGAGGTC 387
Db      601 GCGCACTACAAGCCTGCTTACGCCGCGCATCGACATCAGTGGCATCAACGGGGAGGTC 660
Qy      388 ATGCCGGGGCAG 399
Db      661 ATGCCGGGGCAG 672

```

RESULT 11

```

US-10-425-114-32327
; Sequence 32327, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.

```

APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
PLANTS AND Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 3227
LENGTH: 1605
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: UC-ZMFLB73296F08_FLI
US-10-425-114-32327

Query Match 5.2%; Score 132; DB 17; Length 1605;
Best Local Similarity 100.0%; Pred. No. 2.5e-17;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 268 CAGGACCTTACTACTCGCGCTCGGAGCGGACAAGTCTTACGGCGGGACATCGTGGAC 327
Db 670 CAGGACCTTACTACTCGCGCTCGGAGCGGACAAGTCTTACGGCGGGACATCGTGGAC 729
Qy 328 GCGCACTACAAGGCTGCTTACGCCGGCATCGACATCAGTGGCATCAACGGGGAGGTC 387
Db 730 GCGCACTACAAGGCTGCTTACGCCGGCATCGACATCAGTGGCATCAACGGGGAGGTC 789
Qy 388 ATGCCGGGGCAG 399
Db 790 ATGCCGGGGCAG 801

RESULT 12
US-10-425-115-141081
Sequence 141081, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
PLANTS AND Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 141081
LENGTH: 1638
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_60148C.1
US-10-425-115-141081

Query Match 5.2%; Score 132; DB 18; Length 1638;
Best Local Similarity 100.0%; Pred. No. 2.5e-17;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 268 CAGGACCTTACTACTCGCGCTCGGAGCGGACAAGTCTTACGGCGGGACATCGTGGAC 327
Db 703 CAGGACCTTACTACTCGCGCTCGGAGCGGACAAGTCTTACGGCGGGACATCGTGGAC 762
Qy 328 GCGCACTACAAGGCTGCTTACGCCGGCATCGACATCAGTGGCATCAACGGGGAGGTC 387
Db 763 GCGCACTACAAGGCTGCTTACGCCGGCATCGACATCAGTGGCATCAACGGGGAGGTC 822
Qy 388 ATGCCGGGGCAG 399
Db 823 ATGCCGGGGCAG 834

RESULT 13
US-10-425-115-141084
Sequence 141084, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
PLANTS AND Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 141084
LENGTH: 1800
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(1800)
OTHER INFORMATION: unsure at all n locations
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_60150C.1
US-10-425-115-141084

Query Match 5.2%; Score 132; DB 18; Length 1800;
Best Local Similarity 100.0%; Pred. No. 2.7e-17;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 268 CAGGACCTTACTACTCGCGCTCGGAGCGGACAAGTCTTACGGCGGGACATCGTGGAC 327
Db 604 CAGGACCTTACTACTCGCGCTCGGAGCGGACAAGTCTTACGGCGGGACATCGTGGAC 663
Qy 328 GCGCACTACAAGGCTGCTTACGCCGGCATCGACATCAGTGGCATCAACGGGGAGGTC 387
Db 664 GCGCACTACAAGGCTGCTTACGCCGGCATCGACATCAGTGGCATCAACGGGGAGGTC 723
Qy 388 ATGCCGGGGCAG 399
Db 724 ATGCCGGGGCAG 735

RESULT 14
US-10-767-701-12658
Sequence 12658, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
PLANTS AND Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 12658
LENGTH: 706
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(706)
OTHER INFORMATION: unsure at all n locations
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS54866_1
US-10-767-701-12658

Query Match 4.8%; Score 122.4; DB 18; Length 706;
Best Local Similarity 95.5%; Pred. No. 1.8e-15;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 27, 2005, 07:05:30 ; Search time 1321 Seconds
(without alignments)
11413.763 Million cell updates/sec

Title: US-09-989-739-18

Perfect score: 2547

Sequence: 1 ccattgctcgtaccttcccc.....gctcgtgctgctgcttgcctt 2547

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2547	100.0	2547	12 ADE91329	Ade91329 Maize glu
2	254.2	10.0	1505	6 AAD25704	Aad25704 Maize glu
3	188.8	7.4	664	6 AAD25728	Aad25728 Maize glu
4	107.2	4.2	3001	10 ADE25029	Ade25029 Plant gro
5	103.2	4.1	599	10 ADK54422	Adk54422 Plant DNA
6	103.2	4.1	863	10 ADD17903	Add17903 DNA (Seqi
7	103.2	4.1	863	10 ADK58450	Adk58450 Plant DNA
8	103.2	4.1	1200	2 AAQ05728	Aaq05728 Gene enco
9	101	4.0	281	7 ADS69423	Adsg69423 Corn seed
10	98.6	3.9	693	12 ADJ44656	Adj44656 Plant CDN
11	95.8	3.8	1273	12 ADJ40037	Adj40037 Plant CDN
12	95.2	3.7	1211	10 ADD17881	Add17881 DNA (Seqi
13	95.2	3.7	1211	10 ADK54420	Adk54420 Plant DNA
14	95.2	3.7	1255	2 AAQ05727	Aaq05727 Gene enco
15	92.8	3.6	4464	1 AAN71244	Aan71244 Genomic s
16	92.8	3.6	4465	2 AAQ28697	Aaq28697 Glutamine
17	90.4	3.5	1364	12 ADJ44991	Adj44991 Plant CDN
18	90.4	3.5	1364	12 ADJ44942	Adj44942 Plant CDN
19	88.8	3.5	1584	3 AAC44061	Aac44061 Zea mays
20	88.8	3.5	1673	3 AAC43744	Aac43744 Zea mays

21	85.2	3.4	392	12 ADP94040	Adp94040 Cotton ex
22	85.6	3.4	672	10 ADD17885	Add17885 DNA (Seqi
23	85.6	3.4	672	10 ADK52859	Adk52859 Plant DNA
24	85.6	3.4	1508	13 ADR58314	Adr58314 Cotton CD
25	84	3.3	1297	3 AAC49711	Aac49711 Arabidops
26	84	3.3	1310	3 AAC47011	Aac47011 Arabidops
27	82.4	3.2	1358	3 AAC49538	Aac49538 Arabidops
28	82.4	3.2	1440	3 AAC49542	Aac49542 Arabidops
29	81.8	3.2	729	10 ADD17906	Add17906 DNA (Seqi
30	80.8	3.2	689	10 ADD17880	Add17880 DNA (Seqi
31	80.8	3.2	701	10 ADK54419	Adk54419 Plant DNA
32	80.8	3.2	1061	10 ADD17963	Add17963 cDNA (Seq
33	80.8	3.2	1307	10 ADK54421	Adk54421 Plant DNA
34	80.8	3.2	1317	10 ADD17883	Add17883 DNA (Seqi
35	80.8	3.2	1317	10 ADK58367	Adk58367 Plant DNA
36	80.8	3.2	1362	3 AAC41845	Aac41845 Arabidops
37	80.8	3.2	1362	3 AAC44110	Aac44110 Arabidops
38	80.8	3.2	1444	3 AAC40656	Aac40656 Arabidops
39	80.8	3.2	1519	10 ADD17886	Add17886 DNA (Seqi
40	80.8	3.2	1749	3 AAF13455	Aaf13455 Aspergill
41	80.8	3.2	3895	10 ADK58449	Adk58449 Plant DNA
42	79.8	3.1	599	10 ADD17889	Add17889 DNA (Seqi
43	79.8	3.1	1068	1 AAN71176	Aan71176 Sequence
44	79.8	3.1	1071	12 ADN72200	Adn72200 Thale cre
45	79.8	3.1	1338	1 AAN70758	Aan70758 Sequence

ALIGNMENTS

RESULT 1
ADE91329
ID ADE91329 standard; DNA; 2547 BP.

AC ADE91329;

DT 12-FEB-2004 (first entry)

DE Maize glutamine synthetase (GS1-2) promoter.

XX Maize; cytoplasmic glutamine synthetase promoter; GS1-2 promoter;
KW transgene expression; plant breeding; corn; transgenic; ds.

OS Zea mays.

PN US2003140364-A1.

PD 24-JUL-2003.

PF 20-NOV-2001; 2001US-00989739.

PR 20-NOV-2001; 2001US-00989739.

XX (HINC/) HINCHEY B.

XX (SONG/) SONG H.

XX Hinchey B, Song H;

XX WPI; 2004-020397/02.

PT Novel isolated nucleic acid sequence comprising cytoplasmic glutamine synthetase promoter useful for improving feed or food value, improving processing of corn and products resulting from processing.

PS Claim 11; Fig 2; 62pp; English.

XX The present invention relates to the isolation of maize cytoplasmic glutamine synthetase (GS1-2) promoter. Also disclosed are methods for the expression of transgenes in plants, stably transformed with a selected DNA comprising a maize GS1-2 promoter. The GS1-2 promoter and the methods are useful for plant breeding. The transgenic plant is as a monocotyledonous plant (wheat, maize, rye, rice, oat, barley, turfgrass, sorghum, millet and sugarcane) or dicotyledonous plant (tobacco, tomato,

= instant case

QY 1981 GAAAACTTCATCTTCTGATCTCACACCACATATCCCATTCGCGCTCAACCAACTGATC 2040
DB 1981 GAAAACTTCATCTTCTGATCTCACACCACATATCCCATTCGCGCTCAACCAACTGATC 2040
QY 2041 TAGAAGTTAGATCTTGTAAATAAACAGCTTATTTGAACGATCTCTACTTATATAGTA 2100
DB 2041 TAGAAGTTAGATCTTGTAAATAAACAGCTTATTTGAACGATCTCTACTTATATAGTA 2100
QY 2101 TGTGAAGTGTGCAAGCAGTCCAGCAGCACTAGATAGTTAAGAAATAAATACAGATAG 2160
DB 2101 TGTGAAGTGTGCAAGCAGTCCAGCAGCACTAGATAGTTAAGAAATAAATACAGATAG 2160
QY 2161 ATAAGAGATAGATAAGCAACAGATATATGTATTTAGGATATAGATAGGCAACAGATATATG 2220
DB 2161 ATAAGAGATAGATAAGCAACAGATATATGTATTTAGGATATAGATAGGCAACAGATATATG 2220
QY 2221 CACGCTGGCAGAGATAGATATAGATATAGGACAGATAGAGAGAAATAAATAGCAGAT 2280
DB 2221 CACGCTGGCAGAGATAGATATAGATATAGGACAGATAGAGAGAAATAAATAGCAGAT 2280
QY 2281 AATATATTAAATAGAGATAGATATATTTCTACCACAATCACTACAGTACACATTTACG 2340
DB 2281 AATATATTAAATAGAGATAGATATATTTCTACCACAATCACTACAGTACACATTTACG 2340
QY 2341 AGTGACCGCGATGCGAGTGGAGGACAAACCGTACCGCGCGCTTTCAGAACACTTTCC 2400
DB 2341 AGTGACCGCGATGCGAGTGGAGGACAAACCGTACCGCGCGCTTTCAGAACACTTTCC 2400
QY 2401 AAGCCAGAGCCACTACACCAACCACTCTCGGGCTCTGCTCTATTTATGGAGGAGCAGCC 2460
DB 2401 AAGCCAGAGCCACTACACCAACCACTCTCGGGCTCTGCTCTATTTATGGAGGAGCAGCC 2460
QY 2461 AGCTACAGCTACAGCGTGGGGAAGCAGACACACGATCACTACCTCGCGGCCA 2520
DB 2461 AGCTACAGCTACAGCGTGGGGAAGCAGACACACGATCACTACCTCGCGGCCA 2520
QY 2521 TTGTCCTGCTCGTGGTGTCTCTGCTCT 2547
DB 2521 TTGTCCTGCTCGTGGTGTCTCTGCTCT 2547

RESULT 2
AAD25704
ID AAD25704 standard; DNA; 1505 BP.
AC AAD25704;
XX
DT 12-MAR-2002 (first entry)
XX
DE Maize glutamine synthetase (GSI-2) gene.
XX
KW Maize; transcription regulatory region; nitrogen metabolism; invertase;
KW glutamine synthetase; seed assimilation; seed development; GSI-2 gene;
KW amino acid transaminase; fungal resistance; disease resistance;
KW carbon metabolism; ds.
OS Zea mays.
XX
FH Key Location/Qualifiers
FT misc_feature 1
FT /tag= a
FT /note= "5', deletion start site"
FT 259
FT misc_feature
FT /tag= b
FT /note= "5', deletion start site"
FT 430..439
FT protein_bind
FT /tag= c
FT /bound_moiety= "c-myb transcription factor"
FT 443..448
FT protein_bind
FT /tag= d
FT /bound_moiety= "NIT2 transcription factor"
FT 459
FT misc_feature

FT /tag= e
FT /note= "5', deletion start site"
FT 483..488
FT protein_bind
FT /tag= f
FT /bound_moiety= "NIT2 transcription factor"
FT 500..503
FT /tag= g
FT 593
FT misc_feature
FT /tag= h
FT /note= "5', deletion start site"
FT 603..608
FT /tag= i
FT /note= "P site"
FT 626..631
FT /tag= j
FT 631
FT misc_feature
FT /tag= k
FT /note= "5', deletion start site"
FT 665..767
FT /tag= m
FT 665
FT misc_signal
FT /tag= l
FT /note= "Transcription start site"
FT 768..840
FT exon
FT /tag= n
FT /number= 1
FT 841..1222
FT intron
FT /tag= o
FT /number= 1
FT /cons_splice= (5'site:NO, 3'site:YES)
FT 1223..1262
FT exon
FT /tag= p
FT /number= 2
FT 1263..1469
FT intron
FT /tag= q
FT /number= 2
FT 1470..1505
FT exon
FT /tag= r
FT /number= 3
FT /partial
XX
XX WO200192465-A2.
XX
XX 06-DEC-2001.
XX
XX 23-MAY-2001; 2001WO-US010830.
XX
XX 25-MAY-2000; 2000US-0206984P.
XX
XX (BIOT-) BIOTECHNOLOGY RES & DEV CORP.
XX
XX Muhitch MJ;
XX
XX WPI; 2002-090042/12.
XX
XX New maize glutamine synthase gene promoter, useful for affecting seed
XX assimilation and development (e.g. increasing seed yield and quality) in
XX plants, and for producing plants with increased fungal and disease
XX resistance.
XX
XX Example; Fig 1; 4lpp; English.
XX
XX The invention relates to transcription regulatory region (promoter) for
XX the maize glutamine synthetase (GSI-2) gene. The GSI-2 gene comprising
XX the transcription regulatory region is useful for affecting seed
XX assimilation and development, and for increasing fungal and disease
XX resistance. It is useful for producing plants with reduced mycotoxin
XX levels and increased disease resistance, and for increasing seed yield
XX and quality in plants. It is also useful for encoding proteins involved
XX in seed development and metabolism, particularly enzymes involved in
XX carbon and/or nitrogen metabolism (e.g. glutamine synthetases or their
XX isozymes, amino acid transaminases and invertases). The present sequence
XX is maize GSI-2 gene

PG Pub: 20040148651
— how do I get this?
what IS application #?

```
XX SQ Sequence 1505 BP; 378 A; 394 C; 286 G; 447 T; 0 U; 0 Other;
Query Match 10.0%; Score 254.2; DB 6; Length 1505;
Best Local Similarity 93.6%; Pred. No. 2.2e-45;
Matches 265; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
QY 2265 AAATAAATAGCAGATATATATTAATATAGATAGATATATTTCTACCAACAATCACTA 2324
DB 449 ATAAAGTATAGAGGCACAGATAGATATAGATATATTTCTACCAACAATCACTA 508
QY 2325 CAGTACACATTCAGAGTGCAGCGGATGCAGTCGAGAGGACACCGTACACCGCGCC 2384
DB 509 CAGTACACATTCAGAGTGCAGCGGATGCAGTCGAGAGGACACCGTACACCGCGCC 568
QY 2385 TTGCAGAACACTTTTCCAAAGCCAGAGCCACTACACCAACCACTCTCGGGCTCTGCTCTAT 2444
DB 569 TTGCAGAACACTTTTCCAAAGCCAGAGCCACTACACCAACCACTCTCGGGCTCTGCTCTAT 628
QY 2445 TTATGGAGGAGCAGCAGCTACAGGCTACAGCGGTGGCGAAAGCACACCGGATCAATCA 2504
DB 629 TTATGGAGGAGCAGCAGCTACAGGCTACAGCGGTGGCGAAAGCACACCGGATCAATCA 688
QY 2505 CACTCACATCGCGGCATTTGCTGCTGCTGCTGCTGCTGCTT 2547
DB 689 CACTCACATCGCGGCATTTGCTGCTGCTGCTGCTGCTT 731
RESULT 3
AAD25728
ID AAD25728 standard; DNA; 664 BP.
XX AC AAD25728;
XX DT 12-MAR-2002 (first entry)
XX DE Maize glutamine synthetase (GSI-2) gene transcription regulatory region.
XX KW Maize; transcription regulatory region; nitrogen metabolism; invertase;
KW glutamine synthetase; seed assimilation; seed development; GSI-2 gene;
KW amino acid transaminase; fungal resistance; disease resistance;
KW carbon metabolism; ds.
XX OS Zea mays.
XX FH Key Location/Qualifiers
FT protein_bind 430..439
FT /tag= a
FT /bound_moiety= "c-myb transcription factor"
FT protein_bind 443..448
FT /tag= b
FT /bound_moiety= "NIT2 transcription factor"
FT protein_bind 483..488
FT /tag= c
FT /bound_moiety= "NIT2 transcription factor"
FT CAAT_signal 500..503
FT /tag= d
FT misc_feature 603..608
FT /tag= e
FT /note= "p site"
FT TATA_signal 626..631
FT /tag= f
XX WO200192465-A2.
XX PD 06-DEC-2001.
XX PF 23-MAY-2001; 2001WO-US010830.
XX PR 25-MAY-2000; 2000US-0206984P.
XX PA (BIOT-) BIOTECHNOLOGY RES & DEV CORP.
XX
```

```
PI Muhitch MJ;
XX WPI; 2002-090042/12.
XX New maize glutamine synthase gene promoter, useful for affecting seed
PT assimilation and development (e.g. increasing seed yield and quality) in
PT plants, and for producing plants with increased fungal and disease
PT resistance.
XX Claim 1; Fig 2; 41pp; English.
XX The invention relates to transcription regulatory region (promoter) for
CC the maize glutamine synthetase (GSI-2) gene. the GSI-2 gene comprising
CC the transcription regulatory region is useful for affecting seed
CC assimilation and development, and for increasing fungal and disease
CC resistance. It is useful for producing plants with reduced mycotoxin
CC levels and increased disease resistance, and for increasing seed yield
CC and quality in plants. It is also useful for encoding proteins involved
CC in seed development and metabolism, particularly enzymes involved in
CC carbon and/or nitrogen metabolism (e.g. glutamine synthetases or their
CC isozymes, amino acid transaminases and invertases). The present sequence
CC is maize GSI-2 gene transcription regulatory region
XX SQ Sequence 664 BP; 207 A; 142 C; 112 G; 203 T; 0 U; 0 Other;
Query Match 7.4%; Score 188.8; DB 6; Length 664;
Best Local Similarity 92.1%; Pred. No. 3.3e-31;
Matches 199; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 2265 AAATAAATAGCAGATATATATATATATAGATAGATATATTTCTACCAACAATCACTA 2324
DB 449 ATAAAGTATAGAGGCACAGATAGATAGATATATTTCTACCAACAATCACTA 508
QY 2325 CAGTACACATTCAGAGTGCAGCGGATGCAGTCGAGAGGACACCGTACACCGCGCC 2384
DB 509 CAGTACACATTCAGAGTGCAGCGGATGCAGTCGAGAGGACACCGTACACCGCGCC 568
QY 2385 TTGCAGAACACTTTTCCAAAGCCAGAGCCACTACACCAACCACTCTCGGGCTCTGCTCTAT 2444
DB 569 TTGCAGAACACTTTTCCAAAGCCAGAGCCACTACACCAACCACTCTCGGGCTCTGCTCTAT 628
QY 2445 TTATGGAGGAGCAGCAGCTACAGGCTACAGCGGTGGCGAAAGCACACCGGATCAATCA 2480
DB 629 TTATGGAGGAGCAGCAGCTACAGGCTACAGCGGTGGCGAAAGCACACCGGATCAATCA 664
RESULT 4
ADE25029
ID ADE25029 standard; cDNA; 3001 BP.
XX AC ADE25029;
XX DT 29-JAN-2004 (first entry)
XX DE Plant growth associated gene cDNA seq id 4.
XX KW plant growth; plant growth trait modulation; Brassicaceae; Arabidopsis;
KW Brassica; Zea; Oryza; Triticum; Hordeum; Lolium; Sorghum; Glycine;
KW Medicago; Helianthus; Lactuca; Beta; Vitis; Solanum; Lycopersicon;
KW Capsicum; Gossypium; Hevea; Linum; Prunus; Citrus; Populus; Pinus;
KW Quercus; gene; ss.
XX OS Magnoliophyta.
XX PN US2003188343-A1.
XX PD 02-OCT-2003.
XX PF 07-JAN-2003; 2003US-00338777.
XX PR 09-JAN-2002; 2002US-0347288P.
XX PA (LYNX-) LYNX THERAPEUTICS INC.
```

XX Bowen BA, Haudenschild CD, Buckler ES;
XX WPI: 2003-803305/75.
DR P-PSDB; ADE25059.
XX New isolated or recombinant polypeptide for use in modulating a plant
PT growth trait in a flowering plant e.g. in Arabidopsis, Brassica, Zea, or
PT Oryza.
XX Claim 1; SEQ ID NO 4; 81pp; English.
XX The invention describes an isolated or recombinant polypeptide (I)
CC comprising a sequence: (a) comprising 1 of 30 sequences (S1), as given in
CC the specification, or a conservative variant; (b) encoded by 1 of 30
CC sequences (S2), as given in the specification, or a conservative variant;
CC (c) encoded by a sequence that hybridises under stringent conditions to
CC S2; and (d) encoded by a sequence 70 % identical to S2. The expression or
CC activity of (I) is modulated to modulate a plant growth trait in a
CC flowering plant, of the family Brassicaceae, preferably in a plant that
CC is Arabidopsis, Brassica, Zea, Oryza, Triticum, Hordeum, Lolium, Sorghum,
CC Glycine, Medicago, Helianthus, Lactuca, Beta, Vitis, Solanum,
CC Lycopersicon, Capsicum, Gossypium, Hevea, Linum, Prunus, Citrus, Populus,
CC Pinus, or Quercus. A new method is used to detect genes for a plant
CC growth trait. This sequence represents a plant growth associated cDNA.
XX
SQ Sequence 3001 BP; 836 A; 566 C; 538 G; 1061 T; 0 U; 0 Other;

Query Match 4.2%; Score 107.2; DB 10; Length 3001;
Best Local Similarity 62.2%; Pred. No. 4e-13;
Matches 194; Conservative 0; Mismatches 103; Indels 15; Gaps 1;

QY 102 AGGTTGGGATGAGCAGGATACACCTCTCCAGAGGACACCAAGTGGCTCTCGGT 161
DB 1447 AGGTATGGATTCGAACAGATATACACTTTGTCAGAGGATGTGAATGGCCCTTTGGA 1506

QY 162 TGGCGCTGGGGCTTACCTGGCCCTCAGGTAGATTAGATGGATCTCGTGCCTCCAGG 221
DB 1507 TGGCCCATTTGGTGTCTCCCTGGCCCTCAGGTATCGTTTTCGGAGTTTTTCGT 1566

QY 222 CTCAGCCATATCGATGGCTTTGATCAGCTGACGAATG-----ATCCTG 266
DB 1567 TTGTTTACTGCTCTTTTTCGATTCCTCGTCTCTTGGCTTCTGAATATCTTTGCACTCTT 1626

QY 267 GCAGGACCTTACTACTGCGCGTGGAGCGGACAAAGTCCCTACGGCGGGACATCGTGA 326
DB 1627 GCAGGACCTTACTACTGAGTATTTGGAGCTGACAAATCTTTGGAAGACATTTGTTGA 1686

QY 327 CGCGCACTACAGGCTGCTCTACCGCGCATCGACATCATGTGGCATCAACGGGGAGGT 386
DB 1687 TGCTCACTACAAAGCTCTTTTGTATGCTGGAATCAACATCATGTGGATCAATGGAGAAGT 1746

QY 387 CATGCGGGGCA 398
DB 1747 CATGCGGGGACA 1758

RESULT 5
ADK54422
ID ADK54422 standard; DNA; 599 BP.
XX
AC ADK54422;
XX
XX 06-MAY-2004 (first entry)
XX
XX Plant DNA sequence which confers altered metabolic characteristic #1805.
DE
XX altered metabolic characteristic; plant; acid metabolism;
XX alcohol metabolism; fatty acid metabolism;
XX branched fatty acid metabolism; alkaloid metabolism;
XX amino acid metabolism; ester metabolism; glyceride metabolism;
XX phenolic metabolism; carbohydrate metabolism; sterol metabolism;
XX terpene metabolism; isoprenoid metabolism; alkene metabolism;

KW alkyne metabolism; hydrocarbon metabolism; ketone metabolism;
KW quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.
XX Unidentified.
XX WO2003020936-A1.
XX 13-MAR-2003.
XX 30-AUG-2002; 2002WO-US027884.
XX 31-AUG-2001; 2001US-0316471P.
XX (DOWC) DOW CHEM CO.
XX (DOWC) DOW AGROSCIENCES LLC.
XX Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;
PI Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;
XX WPI; 2003-313091/30.
XX Novel genes that confer altered metabolic characteristics in Nicotiana
PT benchamiana plants, useful for altering the levels of metabolites e.g.
PT acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.
XX Claim 1; SEQ ID NO 1805; 2576pp; English.
PS
XX The invention comprises DNA sequences which confer an altered metabolic
CC characteristic when they are expressed in a plant. The DNA sequences of
CC the invention are useful for producing plants with an altered metabolic
CC characteristic, such as: altered acid metabolism, alcohol metabolism,
CC fatty acid metabolism, branched fatty acid metabolism, alkaloid or other
CC base metabolism, altered amino acid metabolism, altered ester metabolism,
CC altered glyceride metabolism, altered phenolic metabolism, altered
CC carbohydrate metabolism, altered sterol, oxygenated terpene, or
CC isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon
CC metabolism, ketone or quinone metabolism. The DNA sequences of the
CC invention may be used to provide disease resistance in a plant and gene
CC shuffling or sexual PCR procedures. The present nucleic acid represents a
CC DNA sequence of the invention.
XX
SQ Sequence 599 BP; 128 A; 181 C; 179 G; 111 T; 0 U; 0 Other;

Query Match 4.1%; Score 103.2; DB 10; Length 599;
Best Local Similarity 86.4%; Pred. No. 1.7e-12;
Matches 114; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 268 CAGGACCTTACTACTGCGCGTCCGAGCGGACAAAGTCTTACGGCGGGACATCGTGAC 327
DB 271 CAGGACCATACTACTGCGCTCCGCTGCCGAAAGGGCTTCGGCGCGGACATCGTGAC 330

QY 328 CGGCACTACAGGCTGCTCTACCGCGGATCAGATGCGCATCAACGGGGAGTGC 387
DB 331 GCCCACTACAAAGGCTGCACTACGCGGGATCAACATCATGTGGCATCAACGGGGAGTGC 390

QY 388 ATGCGGGGCGAG 399
DB 391 ATGCGGGGCGAG 402

RESULT 6
ADD17903
ID ADD17903 standard; DNA; 863 BP.
XX
XX ADD17903;
XX
XX 15-JAN-2004 (first entry)
XX
XX DNA (SeqID 1971) that confers an altered visual phenotype in plants.
DE ds; visual phenotype; plant; architecture; leaf surface; chlorotic;
KW bleaching; etching; wet leaf; stunting; elongation; texture;
KW agronomic trait; growth regulation; dwarf variety; insect resistance;

DE Gene encoding glutamine synthase in cytosol of rice plant roots.

KW Herbicide-resistance; RGR; ss.

XX Oryza sativa.

XX Key Location/Qualifiers
 FH CDS 59..1132
 FT /*tag= a
 FT /product= "RGR"

XX JP02182190-A.

XX 16-JUL-1990.

XX 16-JUN-1989; 89JP-00154157.

XX 09-SEP-1988; 88JP-00225816.

XX (MITU) MITSUBISHI KASEI CORP.

XX (MITS) MITSUBISHI CORE.

XX (MITS) MITSUBISHI CORP.

XX WPI; 1990-258259/34.

DR P-PSDB; AAR06492.

XX Gene to encode glutamine synthetase - is in cytosol of rice plant leaves and is used for formation of herbicide-resistant plants.

XX Claim 4; Page 3; 16pp; Japanese.

XX The gene was sequenced from a clone isolated from a cDNA library prepd. from the cytosol of rice plant roots. It is useful for the development of herbicide-resistant plants and in the analysis of mechanism of induction by light or gibberellin, and also for analysis of tissue specificity. The protein encoded by the gene is designated RGR and is one of three similar proteins, the others being RGLI (from leaf cytosol) and RGLC (from leaf chloroplasts). See also AAQ05727 and AAQ02729. (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 1200 BP; 287 A; 364 C; 348 G; 201 T; 0 U; 0 Other;

Query Match 4.1%; Score 103.2; DB 2; Length 1200;
 Best Local Similarity 86.4%; Pred. No. 2.2e-12;
 Matches 114; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 268 CAGGACCTTACTTGTGCGCTCGAGGCGACAGTCTACGCGCGGACATCGTGAC 327

Db 518 CAGGACCATCTACTTGTGCGCTCGAGGCGGAAAGGCGTTTCGCGCGGACATCGTGAC 577

QY 328 GCGCACTACAAGCGCTGCTCTACGCGCGCATCGACATCAACGGGGAGGTC 387

Db 578 GCGCACTACAAGCGCTGCTCTACGCGCGGATCAACATCAGTGGCATCAACGGGAGGTC 637

QY 388 ATGCGCGGCGCAG 399

Db 638 ATGCGCGGCGCAG 649

RESULT 9

ADSG9423

ID ADSG9423 standard; cDNA; 281 BP.

XX ADSG9423;

XX 18-NOV-2004 (first entry)

XX Corn seedling-derived polynucleotide (cpds), SEQ ID 4439.

XX Corn; seedling-derived polynucleotide; cdp; ss; plant; seed growth;
 KW seed development; disease resistance; insect infestation; fungal disease;
 KW Bacterial infection; Goss' Bacterial wilt; blight;
 KW Stewart's bacterial wilt; Holcus spot; bacterial leaf blight; leaf spot;

KW bacterial stripe; maize dwarf mosaic virus infection;
 KW environmental stress; water stress; pH stress; temperature stress;
 XX pollution; injury; pesticide.

XX Zea mays.

XX US2003237110-A9.

XX 25-DEC-2003.

XX 06-AUG-2001; 2001US-00923876.

XX 12-MAY-1998; 98US-0085331P.

XX 21-APR-1999; 99US-00298329.

XX (INCY-) INCYTE PHARM INC.

XX Laigudi RV, Ito LY, Sherman BK;

XX WPI; 2002-195165/25.

XX New corn seedling-derived polynucleotides and polypeptides, useful in identifying and altering desired characteristics associated with growth and development, disease resistance, environmental adaptability, quality and yield.

XX Claim 1; SEQ ID NO 4439; 33pp; English.

XX The invention relates to a corn seedling-derived polynucleotide (cdp) selected from ADS64985-ADS71316, or their complements and fragments. Also included are a composition for the detection of altered expression of a cdp (comprising a polynucleotide selected from ADS64985-ADS71316), a method of detecting a polynucleotide in a biological sample using a cdp, a method for using oligomers (and amplification) to recover a regulatory element from a DNA library using oligomers designed against a cdp, a seedling specific regulatory element that regulates the expression of a cdp, an expression vector containing a cdp or regulatory element, a plant transformed with the vector, a host cell containing the vector (and expressing a corn seedling derived protein, CDP), an anti-CDP antibody, identifying a compound which binds a CDP and screening a plurality of compounds for binding to cdp polynucleotide. The cdp polynucleotides, proteins, vectors, cells and antibodies are useful for the identification, evaluation and alteration of seed growth and development, disease resistance (e.g. to insect infestation, fungal disease, bacterial infection, Goss' Bacterial wilt, blight, Stewart's bacterial wilt, Holcus spot, bacterial leaf blight, leaf spot, bacterial stripe and maize dwarf mosaic virus infection) and resistance to environmental stresses (e.g. water stress, pH stress, temperature stress, pollution, injury or pesticides). The present sequence is cdp cDNA sequence.

XX Sequence 281 BP; 54 A; 81 C; 88 G; 56 T; 0 U; 2 Other;

Query Match 4.0%; Score 101; DB 7; Length 281;

Best Local Similarity 85.0%; Pred. No. 3.9e-12;

Matches 113; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 268 CAGGACCTTACTTGTGCGCTCGAGGCGACAGTCTACGCGCGGACATCGTGAC 327

Db 106 CAGGTCCTTACTTGTGGAATCGCGCGGAGAAATCGTTCGGCGGTGACATCGGAC 165

QY 328 GCGCACTACAAGCGCTGCTCTACGCGCGCATCGACATCAGTGGCATCAACGGGGAGGTC 387

Db 166 GCCCCTACAAAGGCTGCTGTACGCGGACATCAACATCAGTGGCATCAACGGGGAGGTC 225

QY 388 ATGCGCGGCGCAG 400

Db 226 ATGCGCGGCGCAG 238

RESULT 10

ADJ44656

ID ADJ44656 standard; cDNA; 693 BP.

XX

CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
CC sorghum, rice or wheat. The polynucleotides and the polypeptides they
CC encode are useful for manipulating crop plants to alter or improve
CC phenotypic characteristics, to produce large quantities of oil or
CC proteins, to incur resistance to insecticides, viruses or fungi, and to
CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
CC have a high nutritional value with reduced apical dominance or dwarfism,
CC early flowering or altered metabolic pathways. This sequence represents a
CC plant nucleic acid of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification but was obtained in
CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 1273 BP; 277 A; 355 C; 377 G; 261 T; 0 U; 3 Other;

Query Match 3.8%; Score 96.8; DB 12; Length 1273;
Best Local Similarity 76.8%; Pred. No. 5.6e-11;
Matches 116; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
QY 263 CTGGCAGGGACCTTACTACTCGCGCTGCGAGCGGACAAAGTCCTACGGCGGGACATCG 322
DB 492 CCTCAGAGGGTCCGTACTACTGTGCGGCGNGGCCNATATAATCGTACGGCGGACATCG 551
QY 323 TGGACGGGCATACAAAGGCTGCTTACGCGGCGATCGACATCATGTCGATCAACGGGG 382
DB 552 TTGATGCCCACTACAAAGGCTGCTTGTTCGCGCATCAACATCAGCGGGATCAACGCAG 611
QY 383 AGGTCATCGCGGGCGAGGTACAGCGTGTGC 413
DB 612 AAGTCATCGCGGGCGAGGCGTGGAGTTC 642

RESULT 12
ADD17881/c
ID ADD17881 standard; DNA; 1211 BP.
XX
AC ADD17881;
XX
XX 15-JAN-2004 (first entry)
XX
DE DNA (SeqID 1949) that confers an altered visual phenotype in plants.
XX ds; visual phenotype; plant; architecture; leaf surface; chlorotic;
KW bleaching; etching; wet leaf; stunting; elongation; texture;
KW agronomic trait; growth regulation; dwarf variety; insect resistance;
KW heat stress; transgenic.
XX Unidentified.
XX WO2003020741-A1.
XX 13-MAR-2003.
XX
PF 30-AUG-2002; 2002WO-US027880.
XX
PR 31-AUG-2001; 2001US-0316326P.
XX
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
XX
PI Crosley R, Skokut T, Ruegger M, Larrinua I, Shukla V;
XX WPI; 2003-300858/29.
XX
PT Novel isolated nucleic acid derived from Nicotiana glauca, Oryza
PT sativa, Saccharum officinarum, and Papaver rhoeas, useful for
PT conferring altered visual phenotypes in plants.
XX
PS Claim 1; SEQ ID NO 1949; 517pp; English.

XX This invention relates to the identification and isolation of novel
CC nucleic acid molecules that confer altered visual phenotypes in plants.
CC Specifically, it refers to modifications of plant architecture and/or

CC leaf surface features in plants, such as chlorotic, bleaching, etching,
CC wet leaf, stunting, elongation and texture phenotypes, which are thought
CC will be agronomic traits beneficial to the farmer. As such, these novel
CC phenotypes can affect growth regulation i.e. useful for creating dwarf
CC varieties, exhibit resistance to insects or heat stress, confer changes
CC in pigment content such that plants have enhanced vitamin production or
CC delayed senescence and also for example produce plants that control the
CC production of ethylene. Furthermore, the present invention comprises
CC generating transgenic plants, as well as reproducibly altering the visual
CC phenotype of plant seeds, plant tissues and plant cells containing the
CC polynucleotides described herein. This polynucleotide is a homologue of a
CC DNA sequence that confers an altered visual phenotype when expressed in
CC plants, the method of the invention.
XX

SQ Sequence 1211 BP; 237 A; 333 C; 363 G; 278 T; 0 U; 0 Other;
Query Match 3.7%; Score 95.2; DB 10; Length 1211;
Best Local Similarity 82.6%; Pred. No. 1.2e-10;
Matches 109; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 268 CAGGACCTTACTACTGCGCGTGGAGCGGACAAAGTCCTACGGCGGGACATCGTGGAC 327
DB 758 CAGGTCCTTACTACTGTGTATCGTGTGCTGACAAAGTCTTTGGCGGTATTTGTTGAC 699
QY 328 GCGCACTACAAAGGCTGCTTACGCGGCGATCGACATCATGTCGATCAACGGGGAGTGC 387
DB 698 TCCCACTACAAAGGCTTGGCTCTATGCGGCGATCAACATCAGTGGATCAACGGCGAGTGC 639
QY 388 ATGCGGGGCGAG 399
DB 638 ATGCGAGGACAG 627

RESULT 13
ADK54420
ID ADK54420 standard; DNA; 1211 BP.
XX
AC ADK54420;
XX
DT 06-MAY-2004 (first entry)
XX
DE Plant DNA sequence which confers altered metabolic characteristic #1803.
XX altered metabolic characteristic; plant; acid metabolism;
KW alcohol metabolism; fatty acid metabolism;
KW branched fatty acid metabolism; alkaloid metabolism;
KW amino acid metabolism; ester metabolism; glyceride metabolism;
KW phenolic metabolism; carbohydrate metabolism; sterol metabolism;
KW terpene metabolism; isoprenoid metabolism; alkene metabolism;
KW alkyne metabolism; hydrocarbon metabolism; ketone metabolism;
KW quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.
XX Unidentified.
XX WO2003020936-A1.
XX 13-MAR-2003.
XX
PF 30-AUG-2002; 2002WO-US027884.
XX
PR 31-AUG-2001; 2001US-0316471P.
XX
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
XX
PI Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;
PI Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;
XX WPI; 2003-313091/30.
XX
PT Novel genes that confer altered metabolic characteristics in Nicotiana
PT glauca plants, useful for altering the levels of metabolites e.g.
PT acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.

XX PS Claim 1; SEQ ID NO 1803; 2576pp; English.

XX CC The invention comprises DNA sequences which confer an altered metabolic

XX CC characteristic when they are expressed in a plant. The DNA sequences of

XX CC the invention are useful for producing plants with an altered metabolic

XX CC characteristic, such as: altered acid metabolism, alcohol metabolism,

XX CC fatty acid metabolism, branched fatty acid metabolism, alkaloid or other

XX CC base metabolism, altered amino acid metabolism, altered ester metabolism,

XX CC altered glyceride metabolism, altered phenolic metabolism, altered

XX CC carbohydrate metabolism, altered sterol, oxygenated terpene, or

XX CC isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon

XX CC metabolism, ketone or quinone metabolism. The DNA sequences of the

XX CC invention may be used to provide disease resistance in a plant and gene

XX CC shuffling or sexual PCR procedures. The present nucleic acid represents a

XX CC DNA sequence of the invention.

SQ Sequence 1211 BP; 278 A; 363 C; 333 G; 237 T; 0 U; 0 Other;

Query Match 3.7%; Score 95.2; DB 10; Length 1211;

Best Local Similarity 82.6%; Pred. No. 1.2e-10;

Matches 109; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 268 CAGGACCTTACTACTGCGCGTGGAGCGGACAAAGTCTTACGGCGGACATCGTGAC 327

Db 454 CAGGTCCTTACTACTGTGGTATCGGTCTGACAAAGTCTTTTGGCGGTGATTTGTTGAC 513

Qy 328 CGCAGCTACAAGGCTGCTCTACGCCGGCATCGACATCAGTGGCATCAACGGGGAGGTC 387

Db 514 TCCCACTACAAGGCTTGCCTCTATGCGGGCATCAACATCAGTGGAAATCAACGGCGAGGTC 573

Qy 388 ATGCCGGGGCAG 399

Db 574 ATGCCAGGACAG 585

RESULT 14

AAQ05727

ID AAQ05727 standard; cDNA; 1255 BP.

XX AC AAQ05727;

XX DT 25-MAR-2003 (revised)

XX DT 02-JAN-1991 (first entry)

XX DE Gene encoding glutamine synthase in cytosol of rice plant leaves.

XX KW Herbicide-resistance; RGSLLI; ss.

XX OS Oryza sativa.

XX FH Key Location/Qualifiers

XX FT CDS 55..1125

XX FT /*tag= a

XX FT /product= "RGSLLI"

XX PN JP02182190-A.

XX PD 16-JUL-1990.

XX PP 16-JUN-1989; 85JP-00154157.

XX PR 09-SEP-1988; 88JP-00225816.

XX PA (MITU) MITSUBISHI KASEI CORP.

XX PA (MITS) MITSUBISHI CORE.

XX PA (MITS) MITSUBISHI CORP.

XX DR WPI; 1990-258259/34.

XX DR P-PSDB; AAR06491.

XX PT Gene to encode glutamine synthetase - is in cytosol of rice plant

XX PT leaves and is used for formation of herbicide-resistant plants.

XX PS Claim 2; Page 2; 16pp; Japanese.

XX CC The gene was sequenced from a clone isolated from a cDNA library prepd.

XX CC from the cytosol of rice plant leaves. It is useful for the development

XX CC of herbicide-resistant plants and in the analysis of mechanism of

XX CC induction by light or gibberellin , and also for analysis of tissue

XX CC specificity. The protein encoded by the gene is designated RGSLLI and is

XX CC one of three similar proteins, the others being RGSR (from root cytosol)

XX CC and RGSC (from leaf chloroplasts). See also AAQ05728 and AAQ02729.

XX CC (Updated on 25-MAR-2003 to correct PA field.)

SQ Sequence 1255 BP; 275 A; 390 C; 335 G; 255 T; 0 U; 0 Other;

Query Match 3.7%; Score 95.2; DB 2; Length 1255;

Best Local Similarity 82.6%; Pred. No. 1.2e-10;

Matches 109; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 268 CAGGACCTTACTACTGCGCGTGGAGCGGACAAAGTCTTACGGCGGACATCGTGAC 327

Db 514 CAGGTCCTTACTACTGTGGTATCGGTCTGACAAAGTCTTTTGGCGGTGATTTGTTGAC 573

Qy 328 GCGCACTACAAGGCTGCTCTACGCCGGCATCGACATCAGTGGCATCAACGGGGAGGTC 387

Db 574 TCCCACTACAAGGCTTGCCTCTATGCCGGCATCAACATCAGTGGAAATCAACGGCGAGGTC 633

Qy 388 ATGCCGGGGCAG 399

Db 634 ATGCCAGGACAG 645

RESULT 15

AA71244

ID AA71244 standard; DNA; 4464 BP.

XX AC AA71244;

XX DT 25-MAR-2003 (revised)

XX DT 06-JUN-1991 (first entry)

XX DE Genomic sequence of alfalfa coding for glutamine synthetase (GS).

XX KW Herbicide-resistant plant cell; Ti plasmid; Agrobacterium tumefaciens;

XX KW phosphinothrican-resistant; enzyme; ss.

XX OS Medicago sativa.

XX FH Key Location/Qualifiers

XX FT repeat_unit 508..521

XX FT /*tag= m

XX FT repeat_unit 541..554

XX FT /*tag= n

XX FT TATA_signal 589..596

XX FT /*tag= o

XX FT misc_RNA 621..740

XX FT /*tag= q

XX FT exon 741..814

XX FT /*tag= a

XX FT exon 1529..1568

XX FT /*tag= b

XX FT exon 1683..1785

XX FT /*tag= c

XX FT exon 2000..2048

XX FT /*tag= d

XX FT exon 2494..2600

XX FT /*tag= e

XX FT exon 2694..2780

XX FT /*tag= f

XX FT exon 3088..3196

XX FT /*tag= g

XX FT exon 3311..3385

XX FT /*tag= h

XX FT exon 3514..3567

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FT      exon      /*tag= i
FT      3703..3740 /*tag= j
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FT      3831..3990 /*tag= k
FT      exon      /*tag= l
FT      4168..4320 /*tag= l
FT      misc_rna   /*tag= r
FT      4321..4530 /*tag= r
FT      polyA_site 4527..4530
FT      /*tag= p
XX
XX PN W08705327-A.
XX
XX PD
XX
XX PD
XX
XX PF 27-FEB-1987; 87WO-US000394.
XX
XX PR 27-FEB-1986; 86US-00833156.
XX
XX PA (GEHO ) GEN HOSPITAL CORP.
XX
XX PI Goodman HM, Donn G;
XX
XX DR WPI; 1987-264124/37.
XX DR P-PSDB; AAP71066.
XX
XX PT Herbicide-resistant plant cells - contg. DNA sequence combination coding
XX PT for over-prodn. of glutamine synthetase.
XX
XX PS Claim 21; Fig 4; 49pp; English.
XX
XX CC The patent application claims plant cells which contain a combination of:
XX CC (a) a genetic sequence coding for genomic GS functional in the plant cell
XX CC ; operably linked to; (b) a genetic sequence capable of increasing the
XX CC levels of expression of GS. The combination is integrated in the genome
XX CC of the plant cell, esp. using a tumour-inducing (Ti) plasmid of
XX CC Agrobacterium tumefaciens as vector, e.g. pGV3850. (Updated on 25-MAR-
XX CC 2003 to correct PA field.)
XX
XX SQ Sequence 4464 BP; 1307 A; 693 C; 756 G; 1718 T; 0 U; 0 Other;
XX
XX Query Match 3.6%; Score 92.8; DB 1; Length 4464;
XX Best Local Similarity 59.0%; Pred. No. 6.5e-10;
XX Matches 196; Conservative 0; Mismatches 132; Indels 4; Gaps 2;
XX
QY 269 AGGGACCTTACTACTGCGCGCTCGGAGCGGACAAAGTCTCTACGGCGGGACATCGTGGACG 328
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2976 AGGGACCATACTATTGTGGAGCTGGTCTGACAAAGGCATTTGGCCGTGACATTTGTGACT 3035
QY 329 CGCACTACAAGCGCTGCTCTACGCGCGCATCGACATCAGTGGCATCAACGGGAGGTCA 388
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3036 CACATTACAAGCCGTCTTTATGTCGGCATCAACATCAGTGGAAATCAATGTTGAAGTGA 3095
QY 389 TGCCGGGGCAGGTACAGCGTGTCTGTAGCTACCTGTCTTTAACTGCACACTGCACCTC 448
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3096 TGCCCTGTCAAGTAAAGTGGACTTATTTACCCCTTTAGCATTTATTTACTACATTTT 3155
QY 449 TGCACACTGCACAGCTAGTAGTATGCTGTATCTCT---GCTGACCCAGGCTTGTTCGTG 505
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3156 TTCAATTTAAATTAACATATGCTGTGATTTTATAAGATTTAAATCTATTGTTTTTTAA 3215
QY 506 GACAGTGGGAGTTCAGAGTCGGCCCTGCGCGCGTCTCGCGCGCGCA-CAGCTTGGGT 564
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3216 TGTAGTGGGAATTCGAAGTTGCTCCCTCAGTTGGTATCTCTGCTGATGATATGGG 3275
QY 565 GGGCTCGGTACTTCTTGGAGAAACGGTAGA 596
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3276 TTGCTCGTTACATTTTGGAGGTAGGTGGACA 3307
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OM nucleic - nucleic search, using sw model

Run on: April 27, 2005, 07:18:36 ; Search time 10814 Seconds
(without alignments)
11412.561 Million cell updates/sec

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Perfect score: 2547
Sequence: 1 ccattggtccgtaccttcccc.....gctcgtgctgctgctt 2547

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_on.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_by.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	254.2	10.0	1505	AF359511	AF359511 Zea mays
C 2	127.2	5.0	78874	AB018107	AB018107 Arabidops
C 3	123	4.8	143681	AC082645	AC082645 Oryza sat
4	122.6	4.8	1369	ZMGS12	X65927 Z mays mRNA
5	118.8	4.7	74968	AB019230	AB019230 Arabidops
6	118.4	4.6	6652	AB037664	AB037664 Oryza sat
C 7	118.4	4.6	161531	AF004880	AF004880 Oryza sat
8	112.2	4.4	1397	AY491968	AY491968 Triticum
C 9	112	4.4	91634	AC148968	AC148968 Medicago
C 10	109.8	4.3	50641	AB008270	AB008270 Arabidops
11	108	4.2	3341	AY491969	AY491969 Triticum
C 12	108	4.2	146568	AC105364	AC105364 Oryza sat
C 13	107.2	4.2	90248	AC026480	AC026480 Arabidops
14	104.8	4.1	1299	AY491970	AY491970 Triticum
15	104.8	4.1	1490	ZMGS14	X65929 Z mays mRNA
16	103.4	4.1	5232	AB0271909	AB0271909 Brassica
17	103.2	4.1	1019	AY339214	AY339214 Zea mays
18	103.2	4.1	1169	OSRIGS8	X14244 Oryza sativ
19	103.2	4.1	1200	E02507	E02507 DNA encodin

20	103.2	4.1	1359	8	ZMGS11	X65926 Z.mays mRNA
21	103.2	4.1	1416	8	MZEGS1D	D14579 Zea mays mR
22	103.2	4.1	1422	8	MZEGS1A	D14576 Zea mays mR
23	102.2	4.0	832	8	AB162423	AB162423 Phyllost
24	102.2	4.0	1350	8	MZEGS1B	D14577 Zea mays mR
25	101.6	4.0	695	8	AB125110	AB125110 Brassica
26	101.6	4.0	1278	8	AY491971	AY491971 Triticum
27	101.4	4.0	7498	8	AB015045	AB015045 Arabidops
28	101.4	4.0	63989	8	AB013393	AB013393 Arabidops
29	100.6	3.9	1317	8	ZMGS13	X65928 Z.mays mRNA
30	96.8	3.8	895	8	ZMGS15	X65930 Z.mays mRNA
31	96.8	3.8	1433	8	MZEGS1C	D14578 Zea mays mR
32	95.2	3.7	1255	6	E02506	E02506 DNA encodin
33	95.2	3.7	1275	8	AB037595	AB037595 Oryza sat
34	95.2	3.7	1276	8	AK061157	AK061157 Oryza sat
35	95.2	3.7	1427	8	AK071969	AK071969 Oryza sat
36	95.2	3.7	1457	8	AK099290	AK099290 Oryza sat
37	95.2	3.7	1494	8	AK063913	AK063913 Oryza sat
38	95.2	3.7	1538	8	AK104987	AK104987 Oryza sat
39	95.2	3.7	1553	8	OSRIGS28	X14245 Oryza sativ
40	95.2	3.7	1556	8	AK109397	AK109397 Oryza sat
41	94	3.7	176965	2	AC148164	AC148164 Zea mays
42	92.8	3.6	4464	8	MSGLNAG	X03931 Medicago sa
43	92	3.6	1625	5	BC064185	BC064185 Xenopus t
44	91.4	3.6	160351	2	AC148152	AC148152 Zea mays
45	90.6	3.6	208685	2	AC145726	AC145726 Zea mays

ALIGNMENTS

RESULT 1
AF359511
LOCUS AF359511 1505 bp DNA linear
DEFINITION Zea mays glutamine synthetase (gs1-2) gene, partial cds.
ACCESSION AF359511
VERSION AF359511.1 GI:19880068
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 1505)
AUTHORS Muhitch,M.J., Liang,H., Rastogi,R. and Sollenberger,K.G.
TITLE Isolation of a promoter sequence from the glutamine synthetase 1-2 gene capable of conferring tissue-specific gene expression in

transgenic maize
JOURNAL Plant Sci. 163 (4), 865-872 (2002)
REFERENCE 2 (bases 1 to 1505)
AUTHORS Muhitch,M.J., Liang,H., Rastogi,R. and Sollenberger,K.G.
TITLE Direct Submission

JOURNAL Submitted (12-MAR-2001) Mycotoxin Research Unit, NCAUR, ARS, USDA, 1815 N. University St., Peoria, IL 61604, USA
FEATURES
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626..>1505
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TATA_signal
mRNA

CDS

filing date 11-20-2001

not
Pub 15/1/01
Cmml:abp/abp
1/01

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Best Local Similarity 93.6%; Pred. No. 7.5e-41;
Matches 265; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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Db 449 ATAAATAGAGGACAGATAGATATAGATAGATATATTTCTACCAACAATCACTA 508

Qy 2325 CAGTACAACTTACGAGTGACCGCGGATGACGATCGAGAGGACAAACCGTACCAACGGGCC 2384
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Db 509 CAGTACAACTTACGAGTGACCGCGGATGACGATCGAGAGGACAAACCGTACCAACGGGCC 568

Qy 2385 TTGCAGACACTTCCAAAGCCAGACGACCTACACCAACCACTTCGGGCTCTGCTCTAT 2444
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Db 569 TTGCAGACACTTCCAAAGCCAGACGACCTACACCAACCACTTCGGGCTCTGCTCTAT 628

Qy 2445 TTATGGAGGACGACGACGACCTACAGCTACAGCCGTGGCGAAAGCACACCGATCAATCA 2504
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Db 629 TTATGGAGGACGACGACGACCTACAGCTACAGCCGTGGCGAAAGCACACCGATCAATCA 688

Qy 2505 CACTCACTCGCGGCAATGCTGCTGCTGCTGCTGCTGCTGCTT 2547
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Db 689 CACTCACTCGCGGCAATGCTGCTGCTGCTGCTGCTGCTGCTT 731

RESULT 2
AB018107/c
LOCUS      AB018107.1 GI:3702722
DEFINITION Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K12B20.
ACCESSION AB018107 BA000015
VERSION   AB018107.1 GI:3702722
KEYWORDS
SOURCE    Arabidopsis thaliana (thale cress)
ORGANISM  Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
REFERENCE 1 Kaneko, T., Katoh, T., Sato, S., Nakamura, Y., Asamizu, E., Kotani, H.,
          Miyajima, N. and Tabata, S.
          Structural analysis of Arabidopsis thaliana chromosome 5. IX.
          Sequence features of the regions of 1,011,550 bp covered by
          seventeen Pl and TAC clones
          DNA Res. 6 (3), 183-195 (1999)
JOURNAL   DNA Res. 6 (3), 183-195 (1999)
MEDLINE   99397451
PUBMED    10470850
REFERENCE 2 (bases 1 to 78874)
AUTHORS   Nakamura, Y.
TITLE     Direct Submission
JOURNAL   Submitted (08-OCT-1998) Yasukazu Nakamura, Kazusa DNA Research
          Institute, Department of Plant Gene Research; 1532-3, Yana,
          Kisarazu, Chiba 292-0812, Japan (E-mail: ynakamu@kazusa.or.jp,
          Tel: 81-438-52-3935, Fax: 81-438-52-3934)
COMMENT   Address for correspondence: kaos@kazusa.or.jp
          For the latest information on annotation of this clone, please see
          http://www.kazusa.or.jp/kaos/cgi-bin/agg_graph.cgi?c=k12B20
          Genes with similarity to proteins in the databases are described in
          'product' or 'note' qualifiers. Genes that have no significant
          protein similarity are described as 'unknown protein'.
          The software programs used to predict genes include: Grail
          (Informatics Group, Oak Ridge National Laboratory,
          http://compbio.ornl.gov/Grail-1.3/),
          GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
          NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
          Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
          SplicePredictor (Volker Brendel, Stanford University,
          http://gremlin1.zool.iastate.edu/cgi-bin/ap.cgi).

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Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be
shorter because we remove overlaps between neighboring submissions.
The 5' clone is MPA22 and the 3' clone is T31G3.

FEATURES
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/ecotype="Columbia"
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/notes="CDS is reported in Acc# AB025630
gene_id:MPA22.9
unknown protein"
/number=1
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EKIYCPYRCSMLMSTELSEAEQSNVRACIKSELFCIDCKVPWHSLSADYKRI
HSRLVNDMLKVLANDQMRQCSECKHMLTEGCGNHITCRGCEYFCYCGCHKWTKY
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LFSARKVFGEMPERNAVSTALVAVYKGELEAKSMFDLMPERNLGSNNALVDGLV
KSGDLVNAKLFDEMFKRDIISYMSIDGYAKGDMVVSARDLFEERAGVDYRAWSALI
LGYAQGNPNEAFKVFSEMCAKNVQDEFIMVGLMSACQSQMGCELCCEKVDVSYLHQRM
NKFSHYVVPALIDNNAKCHMDRAAKLFEEMPQDRLVSYCSMMEGMAIHGCGSEAIR
LLEKMWDEGIVPDEVAFTVLKVGQSLVEEGLRFLVLMKRYKSYLASPDHYSCIVN
LLSRGTGLKEAYELIKSMPEAHASAGSLGCSLGHNTKEIAEVAWHLFELEPQSA
GSVLLSNLYAALDRWTDVAHLDRKNENIGITKICGRSWISR"
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QNDYGGHRTNHLSDRLWILLSQOALLGFCNGTVLAEDSMKSGDNDESGNTG
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IGADKSGRDVVDVSHYKALVAGINISGINGEVMFGOWEFOVGPAGVISAADITWAR
YILERTIELAGVYVDFPKPIPGDWNGAGAHCVSTKSMREEGGVEILKALDKLGR
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CDS

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CLQCNFMHRCQIDLPVRININRHDHRSITRIRHGKIGCKVCKRKMVDGFGYICV
KCLSFARHACATRDVEMVVELEGTEDEIGPEVIDDNTIKFSDHNLRLNNDG
DQQLIHENIACEALQILSEPPFYSCQCNFKLQKCANHPKHKHVRNLPFTLLTS
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CGKDSVPRCDECDYGLGKCALLPGKMNRYDDHPLFLSFDEMYDGEWCEACET
KVNSEMYFCNDCGTLILHSCVGVDFSYIKHSHLMNIRKVVSNISICRPPCFVCNR
CKPFSILKLSKGVNVYICSPKRLTY"
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29612..29709,30417..31079,31426..31940,32022..32082,
32169..32438,32552..32813,32936..33249)
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CDS

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SKAFVPLVRMWPMDIGINTSSSYVSNRRKRAVOVSRFLOMMQTPILYKKEETGEPE
PSEQNVTKLKLKLLSLADSVRSEKOLLKEVPVLQHLKSLDACPSELTOQDANSIF
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CDS

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Matches 199; Conservative 0; Mismatches 98;

Qy 103 GGTTCGGGATTGACGAGGATACACCCCTTCTCCAGAAGACACCAAGTGGCCTCTCGGTT 162
Db 15309 GGTATGGTATTGACAGAATACACTTTACTCCAGAAGATGTGAAGTGGCCTGTGGTT 15250

Qy 163 GGCCGCTTACGGCGGCTACCCCTGAGGTAGATAGATGATCT---GGTGCCTCCA 219
Db 15249 GGCCTATTGGTGGTTATCCCGGCCCTCAGGTGAAGAAGATGATATAATCGGTTTGT 15190

Qy 220 GGCTCCAGCCATATCGATGGCTTTGATCAGCTGACGGAATGATCTCGCAGGACCTTAC 279
Db 15189 ATCTTTTCGTTGCGGTATTCTTAAATTTTGGCGAAATATGATTGCAGGACCGTAC 15130

Qy 280 TACTGCGCGTCGCGAGCGGACAAAGTCTTACCGGCGGACATCGTGGACCGCAGCTACAAG 339
Db 15129 TATTGCGGTATTGAGCAGACAAATCTTTTGCAGAGATGTTGTTGATCTCACTACAAG 15070

Qy 340 GCCTGCCTTACGCGCGCATCGATCATGTCGATCAACGGGAGGATCATGCCGGGGCAG 399
Db 15069 GCCTGCTTATACGCTGGGATCAACATTAGTGGCATCAATGGAGAAGTCAATGCCGGGTCAG 15010

RESULT 3
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LOCUS Oryza sativa chromosome 3 BAC OSJNB0033N16 genomic sequence,
DEFINITION complete sequence.
ACCESSION AC082645
VERSION AC082645.13 GI:13249436
KEYWORDS HTG.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretidae; Oryzae; Oryza.
REFERENCE 1 (bases 1 to 143681)
Buell, C.R., Yuan, Q., Ouyang, S., Moffat, K.S., Hill, J.N., Burr, P.C.,
Hsiao, J., Zismann, V., Pai, G., Bowman, C.L., Fujii, C.Y.,
VanAken, S.E., Bowman, C.L., Craven, B., Utterback, T.R., Khalak, H.,
Feldblum, T.V., Quackenbush, J., White, O., Salzberg, S.L. and
Fraser, C.M.
Oryza sativa chromosome 3 BAC OSJNB0033N16 genomic sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 143681)
Buell, R.
Direct Submission
JOURNAL Submitted (29-SEP-2000) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
REFERENCE 3 (bases 1 to 143681)
Buell, R.
Direct Submission
JOURNAL Submitted (08-MAR-2001) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
REFERENCE 4 (bases 1 to 143681)
Buell, R.

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repeat_region complement(26630..26686)
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Best Local Similarity 63.8%; Pred. No. 5.6e-14;
Matches 220; Conservative 0; Mismatches 120; Indels 5; Gaps 2;
QY 253 ACGGAATGATCTGCGAGGACCTTACTCTGCGCGGTGCGAGCGGACAGTCTTACGGG 312
DB 123696 ACGAAATGGTGTAGTGGTCCGACTCTGCGCGGCGGAGCGGACATAATCGTACGGG 123637
QY 313 CGGGACATCGTGGCGGACCTACAGGCTGCGCTTACGCGCGGATCGACATCAGTGGC 372
DB 123636 CGCGACATCGTGTATGCCACTACAGGCTGCGCTTATGCGGATCAACATCAGCGG 123577
QY 373 ATCAACGGGAGGTGATCGCGGCGGAGGTACAGCGTGTCTTACGTACCTTGTCTTTA 432
DB 123576 ATCAACGGAGAGTCAATCGCGGCGGAGGTAGAACATTTCTGAATTTCTGCACACCT--- 123520
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DB 123519 -CGCGTTTCTGCGCAATTTTTTTCGCGACACTTTGTCATGAGCTGATCGCTTGTAT 123461
QY 493 AGCGTTGTTGCGGACAGTGGAGTTCAGGTCGCGCTGCGCTGCGCTGCGCTGCGCTGCG 552
DB 123460 GTGCGATTTGTGACAGTGGAGTTCAGATTTGCGCTGCTGCTGCTGCTGCTGCTGCG 552
QY 553 GA-CAGCTTGGTGGGCTCGCTACATTTCTTGAGGAAACGGTAGA 596
DB 123400 GATCATGCTGGTGGCAGCTACATTTCTTGAGGTAGACTGAAA 123356

RESULT 4
LOCUS ZMG512 1369 bp mRNA linear PLN 09-DEC-1993
DEFINITION 2.mays mRNA gel-2 for glutamine synthetase.
ACCESSION X65927
VERSION X65927.1 GI:434325
KEYWORDS glutamine synthetase.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1369)
AUTHORS Li.M.G., Villemur,R., Hussey,P.J., Silflow,C.D., Gantt,J.S. and
Snustad,D.P.
TITLE Differential expression of six glutamine synthetase genes in Zea
mays
JOURNAL Plant Mol. Biol. 23 (2), 401-407 (1993)
MEDLINE 9403318
PUBMED 8106013

REFERENCE 2 (bases 1 to 1369)
AUTHORS Snustad,P.D.
TITLE Direct Submission
JOURNAL Submitted (28-APR-1992) P.D. Snustad, University of Minnesota, Dept
of Genetics & Cell Biology, College of Biological Sciences, 250
BioSciences Center, 1445 Gortner Ave/St Paul MN 55108-1095, USA
COMMENT See also X65926-31.
FEATURES Location/Qualifiers
source 1..1369
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/mol_type="mRNA"
/strain="inbred line A188"
/db_xref="taxon:4577"
/clone_lib="pGS1-2"
/clone_lib="lambda gt10; Gantt"
/dev_stage="seedling"
1..1369
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103..1209
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/db_xref="GI:434326"
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PSNRGRGAALIPSHPDVKAEPFGEIORYTLLOKDTKPLGWLAYLPGPGQPYTCAA
GADSKYGRDVIDCAYKACIAGIDISINGEIMFQWFEVAPAVGAGDQLWVARY
ILERITRIAGVVSFDPKPIPDGWNAGAHNTYTSKMSRSDGGEVIKKAIGKLGRH
REHIAAYGDGNERPLTGRHETADINTFVWGVPNRGASVRVGRDTEKEGKGYEDRRPA
SNMDPVYVVTCLIAETITMLWEPSSHNGDGKGAAP"
ORIGIN
Query Match 4.8%; Score 122.6; DB 8; Length 1369;
Best Local Similarity 87.6%; Pred. No. 3.2e-14;
Matches 134; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 247 CAGCTGACGGAATGATCTCTGCGAGGACCTTACTCTGCGGTGCGGAGCGGACAGTCC 306
DB 538 CCGTGTGTTGATCTCTGCGGCTTCTGCGGCTTCTGCGGCTTCTGCGGCTTCTGCGGCTT 597
QY 307 TACGCGCGGACATCTGCGGACGCGGACGCGGACGCGGCTTCTGCGGCTTCTGCGGCTTCT 366
DB 598 TACGCGCGGACATCTGCGGACGCGGACGCGGCTTCTGCGGCTTCTGCGGCTTCTGCGGCTT 657
QY 367 AGTGGCATCAACGGGAGGTCTGCGGCGGCGAG 399
DB 658 AGTGGCATCAACGGGAGGTCTGCGGCGGCGAG 690

RESULT 5
LOCUS AB019230 74968 bp DNA linear PLN 14-FEB-2004
DEFINITION Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MBBS.
ACCESSION AB019230 BA000014
VERSION AB019230.1 GI:3869069
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1
AUTHORS Sato,S., Nakamura,Y., Kaneko,T., Katoh,T., Asanizu,E. and Tabata,S.
TITLE Structural analysis of Arabidopsis thaliana chromosome 3. I.
Sequence features of the regions of 4,504,864 bp covered by sixty
P1 and TAC clones
JOURNAL DNA Res. 7 (2), 131-135 (2000)
MEDLINE 20277480
PUBMED 10819329
REFERENCE 2 (bases 1 to 74968)

333-399

AUTHORS Sato, S., Nakamura, Y., Kaneko, T., Kato, T., Asanizu, E. and Tabata, S.
 TITLE Direct Submission
 JOURNAL Submitted (29-OCT-1998) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan [E-mail: ynakamu@kazusa.or.jp, Tel: 81-438-52-3935, Fax: 81-438-52-3934]
 COMMENT Address for correspondence: kaos@kazusa.or.jp
 For the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgi-bin/aggd_graph.cgi?c=MEB5
 'product' with similarity to proteins in the databases are described in 'genes' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'.
 The software programs used to predict genes include: Graal (Informatics Group, Oak Ridge National Laboratory, <http://compbio.ornl.gov/Graal-1.1.3/>), GENSCAN (Chris Burge, MIT, <http://CCR-081.mit.edu/GENSCAN.html>), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, <http://www.cbs.dtu.dk/services/NetGene2/>), SplicePredictor (Volker Brendel, Stanford University, <http://gremlini.zoology.illstate.edu/cgi-bin/sp.cgi>).
 Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, <http://genome.wustl.edu/eddy/tRNAscan-SE/>).
 This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is MIG5 and the 3' clone is MEG14.
 FEATURES
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 /translation="MASMSPALNRFSGLSKTTLSADFPSSRRSFUPPTRVGUKISS AASEBPLSVTVNGLKMPNPFVIGSGPGNTYTMKRAFDEGWGAVIAKTVSLDASKV INVTPLYRLRTSGNSGAKTDVIGWONIELISDRPLETLMKEAFGLKEYVDRILIAS VMEYNTKAWEEILDRVEQGVDALEINFSCPHGMPERRMGAAVGQDALLDRPCGWI NAKATVPWAKMTPNITDIPARVSLKSCGEGIAALNTIMSVMGIDMKTLDRPCQVK GYSTPGYSYKAVRPALAKVMNIAMKMKSEFSEDRLSGIGVETGYDAAEFILGS NTVOVCTGVMMHGYGHVKTLCABKDFMKQHNFTIEBFGRHSLQYFTTTHTDLVKRQK EAYVQKRAEKRLGSKDKMTGDFGFKETESVSN"
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359 TCGACATCAGTGGCATCAACGGGAGGTTCATCGCGGCGAGTACAGCGTCTGCTCTAG 418
 4733 TCAACATCAGTGGATCAACGGCGAGGTTCATCGCGGCGAGTGAACACTACTCTCAAC 4792
 419 CTACCTTGTCTTTAACTGCACACTGCATCTGCACACTGCACAGCT----- 464
 4793 CTTCGCAATTTCTATCGTCTTGAATAGTGGAGTACATTTCTGACCATGCTAAATATCGTA 4852
 465 --AGTAGTATCTGCTATCTCTGCTGACCCAGGCTTGTTCGTGACAGTGGAGTTCAG 522
 4853 TCAGATCTATAAATGGTAATGTTATTAACATTTGTGATCGCGTCTTTTCAGTGGAGTCCAA 4912
 523 GTGCGCCCTGCGCTCGGCTCTCGCGCGGCA-CAGCTTGGTGGGCTCGCTACATCTT 581
 4913 GTTGGCCGCTGCTCGGCAATTTCTGCGCGTATCAGGTGGTGGTTCGCTACATCTT 4972
 592 GAGGAA 587
 4973 GAGGTA 4978

RESULT 7
 AP004880/c
 LOCUS
 DEFINITION Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 2, PAC clone: P0487D09.
 ACCESSION AP004880
 VERSION AP004880.3 GI:46390424
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
 1 Sasaki, T., Matsumoto, T. and Yamamoto, K.
 Oryza sativa nipponbare (GA3) genomic DNA, chromosome 2, PAC clone: P0487D09
 Published Only in Database (2002)
 2 (bases 1 to 161531)
 Sasaki, T., Matsumoto, T. and Yamamoto, K.
 Direct Submission
 Submitted (20-MAR-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kamondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
 (E-mail: tsasakienae.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/, Tel: 81-298-38-7441, Fax: 81-298-38-7468)
 On Apr 14, 2004 this sequence version replaced gi:33235578.
 Genes were predicted from the integrated results of the following: GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), FGENESH (http://www.softberry.com/), GeneMark.hmm (http://opal.biology.gatech.edu/GeneMark/), GlimmerM (http://www.tigr.org/tdb/glimmerm/glmr.form.html), RicheHM (http://rgp.dna.affrc.go.jp/RicheHM/), SplicePredictor (http://bioinformatics.iastate.edu/cgi-bin/sp.cgi), sim4 (http://globin.cse.psu.edu/html/docs/sim4.html), gap2 (http://www.tigr.org/software/glimmer/), BLASTN and BLASTX. The genomic sequence was searched against NCBI NonRedundant Protein database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP or DBJ. Protein homologues of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP. ESTs represent the identified cDNA sequences using BLASTN with the corresponding DBJ accession no. and RGP clone ID. Full-length cDNAs represent the identified cDNA sequences using BLASTN with the corresponding DBJ accession no.
 A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with full-length cDNA or EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard. A gene

predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence.
 The orientation of the sequence is from SP6 to T7 of the PAC clone. This sequence of P0487D09 clone has an overlap with P0643A10 (DBJ: AP005319) clone at 5' end and with P0694F11 (DBJ: AP005112) at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at
 http://rgp.dna.affrc.go.jp/GenomeSeq.html.

FEATURES
 source

1. 161531
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 /mol_type="genomic DNA"
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 /db_xref="taxon:39947"
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 /clone="P0487D09"
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 complement(3315..6553)
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 /protein_id="BAD15888.1"
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LOCUS	AB008270	50641 bp	DNA	linear	PLN 14-FEB-2004			
DEFINITION	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MTG13.							
ACCESSION	AB008270	BA000015						
VERSION	AB008270.1	GI:2618604						
KEYWORDS								
SOURCE	Arabidopsis thaliana (thale cress)							
ORGANISM	Arabidopsis thaliana							
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosid II; Brassicales; Brassicaceae; Arabidopsids.							
	1 Nakamura,Y., Sato,S., Kaneko,T., Kotani,H., Asamizu,E., Miyajima,N. and Tabata,S.							
AUTHORS	Structural analysis of Arabidopsis thaliana chromosome 5. III. Sequence features of the regions of 1,191,918 bp covered by seventeen physically assigned P1 clones							
	DNA Res. 4 (6), 401-414 (1997)							
JOURNAL	98162728				CDS			
MEDLINE	9501997							
PUBMED	2 (bases 1 to 50641)				CDS			
REFERENCE	Nakamura,Y.							
AUTHORS	Direct Submission				CDS			
Submitted (24-OCT-1997) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)								
TITLE	Address for correspondence: kaos@kazusa.or.jp				CDS			
For the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MTG13								
JOURNAL	Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'.				CDS			
The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/Grail-1.3/), GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and SplicePredictor (Volker Brendel, Stanford University, http://grmln1.zool.iastate.edu/cgi-bin/sp.cgi).								
FEATURES	Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE/).							
	This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is MQK4 and the 3' clone is F5E19.							
	Location/Qualifiers							
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CDS	/ecotype="Columbia"							
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	/db_xref="GI:10176966"							
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CDS	complement(join(10396..10528,10717..10847,10895..11019,11247..11470,11565..11683,11773..11990,12108..12183))							

/note="unnamed protein product; contains similarity to	
beta-glucosidase	
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Qy	373	ATCAACGGGGAGGTATCGCGGGGAGGTACAGCGTGTCTGTCTAGCTACCTTGTCTTTTA	432
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Qy	433	ACTGCACACTGCATCTCTGCACACTGCACAGTACTAGTACTGTCTCTCTCTGCTGACCC	492
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Qy	493	AGGCTTGTTCGTGGACAGTGGGAGTTCCAGGTGCGGCCCTCGCGGTCTCGGCCCGGC	552
Db	7502	AGCTTGTGTGGTTCAGTGGGAGTTCCAAAGTCGGTCCACCGTTGGATCGTCTGCCGCC	7443
Qy	553	GA-CAGCTTGGGTGGGCTCGCTACATCTTTGAGGAAAAACGGTAGACCTGCCCTCGCG	610
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JOURNAL			
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gene			
mRNA			
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Best Local Similarity			
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Db	7900	TATTGAATTCAGGTACGGAATTAACAAAGATATACCTTCTTCCAAAGGATTAAGT	7841
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Db	7840	GGCCGGTAGGTTGGCCGGTCGCGGTTTCCAGGTCCTCAGGTAAACTTCTCCACGCA	7781
Qy	197	TTAGATGATCTGCGTGGCTCCAGGCTCCAGCCATATCGATGGCTTTGATCAGCTGACGG	256
Db	7780	TCAAACTAAATCCATATTGACCTCAACACTAAATTTCTTTTATAAAAAAGAACAAAT	7721
Qy	257	AATGATCTCTGG----CAGGACCTTACTACTGCGCGCTCGGAGCGGCAAGTCTCTACGGG	312

trnAscan-SE (Sean Eddy, <http://genome.wustl.edu/eddy/trnAscan-SE/>).
Simple repeats are identified by repeatmasker (Arian Smit,
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>).

FEATURES
Source

Location/Qualifiers

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mRNA

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SGYVDDDEHGEWFLYTGSGRDLGNGKRVNKIOSDOAKPKMNEALRLSCMGYVVR
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GKLTCLCRSKIPIHVAKNPRINLALYSAILANVTKCSGEATKAVHHIIRNODRPD
KAFTERAVTKGANAASGVLSGESWEDROBQWGVHFFHVAGIAGAAVGAQSVAL
SGYVDDDEHGEWFLYTGSGRDLGNGKRVNKIOSDOAKPKMNEALRLSCMGYVVR
VRSSEKRSAYAPAEGRVDGYVRIEKCNSVGVQGLHKMCRVLFYRCNDEPAPWTS
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KKNRKAKGNNAKRLLEKFSQICRKLVSPLVPTTCAHNFCAKCLAEFAGITQLR
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gene

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/note="contains PF00097: Zinc finger, C3HC4 type (RING finger)"
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/note="contains PF00097: Zinc finger, C3HC4 type (RING finger)"
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/note="contains PF00097: Zinc finger, C3HC4 type (RING finger)"
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QY 162 TGGCGCTGGGGGCTACCTCGCCCTCAGGTAGATAGATGATCGTGCCTCCAGG 221	
Db 82075 TGGCCCATTTGGTGGCTTCCCTGGGCCCTCAGTACATTCCTGCGGAGTATTTTCGT 82016	
QY 222 CTCAGCCCATATCATGGCTTTGATCAGCTGACGGAATG-----ATCCTG 266	
Db 82015 TTGTTACTGCTCTTTTCGATTCTCCGTTCTTGCTTCTGAATTATCTTTCGACTCTT 81956	
QY 267 GCAGGACCTTACTCTGCGCGCTGGAGCGGACAAAGTCTTACCGGGGGACATCGTGGGA 326	
Db 81955 GCAGGACCTTACTCTGAGTATTTGGAGCTGACAAATCTTTTGGAGAGACATTGTGA 81896	
QY 327 CGCGCACTACAGGCGCTCTACGCGGCATCGACATCAGTCAGTCATCAACGGGGAGGT 386	
Db 81895 TGCTACTACAAAGCCTCTTTGTATGCTGGAAACAACATCAGTGGGATCAATGAGAAGT 81836	
QY 387 CATGCCGGGGCA 398	
Db 81835 CATGCCGGGACA 81824	
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LOCUS	AY491970 1299 bp DNA linear PLN 28-DEC-2003
DEFINITION	Triticum aestivum glutamine synthetase isoform GSe1 (GS) gene, complete cds.
ACCESSION	AY491970
VERSION	AY491970.1 GI:40317419
KEYWORDS	Triticum aestivum (bread wheat)
SOURCE	Triticum aestivum
ORGANISM	Triticum aestivum
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
AUTHORS	Dionisio,G., Jahn,T.P. and Schjoerring,J.K.
CONSRM	Plant Biotechnology Consortium (DK)
TITLE	Cloning of wheat glutamine synthetase isoforms by functional complementation and RACE PCR
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1299)
AUTHORS	Dionisio,G., Jahn,T.P. and Schjoerring,J.K.
CONSRM	Plant Biotechnology Consortium (DK)
TITLE	Direct Submission
JOURNAL	Submitted (01-DEC-2003) Plant Nutrition, The Royal Veterinary and Agricultural University (KVL), Thorvaldsensvej 40, Frederiksberg C, Copenhagen DK-1871, Denmark
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Query Match	
Best Local Similarity	
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QY 328 GCGCACTACAAGCGCTCGCTCTACGCGGCATCGACATCAGTCGATCAACGGGGAGGTC 387	
Db 601 GCGCACTACAAGCGCTCGCTCTACGCGGCATCAACATCGCGGCATCAATGCAGAGTC 660	
QY 388 ATGCCGGGGCAG 399	
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DEFINITION	Z.mays mRNA gsl-4 for glutamine synthetase.
ACCESSION	X65929
VERSION	X65929.1 GI:434329
KEYWORDS	glutamine synthetase.
SOURCE	Zea mays
ORGANISM	Zea mays
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
AUTHORS	1 (bases 1 to 1490)
TITLE	Differential expression of six glutamine synthetase genes in Zea mays
JOURNAL	Plant Mol. Biol. 23 (2), 401-407 (1993)
MEDLINE	94033318
PUBMED	8106013
REFERENCE	2 (bases 1 to 1490)
AUTHORS	Snustad,P.D.
TITLE	Direct Submission
JOURNAL	Submitted (28-APR-1992) P.D. Snustad, University of Minnesota, Dept of Genetics & Cell Biology, College of Biological Sciences, 250 BioSciences Center, 1445 Gortner Ave/St Paul MN 55108-1095, USA
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 27, 2005, 14:24:46 ; Search time 8062 seconds
(without alignments)
12025.514 Million cell updates/sec

Title: US-09-989-739-18
Perfect score: 2547
Sequence: 1 ccattgctccgtacctcccc.....gctcgtcgtcgtcgtcgtc 2547

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	587.6	23.1	951	9	CG115681
2	562.2	22.1	797	8	CC343195
3	561.2	22.0	796	9	CG014631
4	551.2	21.6	800	9	CC607969
5	546.8	21.5	876	9	CG999928
6	540.6	21.2	974	8	CC013698
7	538	21.1	681	9	CC937355
8	502	19.7	860	9	CC363992
9	501.8	19.7	802	9	CC221794
10	485.2	18.3	627	9	CG891370
11	460.6	18.1	888	9	CG213069
12	420.6	16.5	937	9	CG115678
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14	288.6	11.3	737	8	B2401579
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17	259	10.2	625	8	B2406372
18	254.2	10.0	647	8	B2365761
19	254.2	10.0	765	8	B2373733
20	254.2	10.0	796	8	B2810088
21	239	9.4	510	9	CC727481
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23	175.8	6.9	765	8	B2719724
24	172.6	6.8	348	8	B2412338

ALIGNMENTS

RESULT 1
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DEFINITION genomic survey sequence.
ACCESSION CG115681
VERSION CG115681.1 GI:33999118
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE 1 (bases 1 to 951)
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, O. and
Bennetzen, J.
Maize Genomics Consortium
Unpublished (2003)
Other GSSs: PU0GP86TB
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: Sheared ends.
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Db 105 CCATGGTCCGTACCTTCCCTGCTGCACGAAATGAACCGACCTGTTGCGTACAGACATT 164


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Qy 715 GGAT-ACCGAGATCCCGCGGTGGTGTCTTCTCGACCCCAA--CCAATTGGGTGACCA 771
Db 95 GGATCACCAGATCCCGCGGTGGTGTCTTCTCGACCCCAAAGCCAATTCCGGTGACCA 36
Qy 772 -TTGCTACCAACAATTTTGGGTTTGGATATGTGG 805
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DEFINITION genomic survey sequence.
ACCESSION CG014631
VERSION CG014631.1 GI:33886796
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 796)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Contact: Cathy Whitelaw
TIGR
712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.

FEATURES
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Db 95 GGATCACCAGATCCCGCGGTGGTGTCTTCTCGACCCCAAAGCCAATTCCGGTGACCA 36
Qy 772 -TTGCTACCAACAATTTTGGGTTTGGATATGTGG 805
Db 35 TTTCGCTACCAACAATTTTCGGTTTGGATATGTGG 1

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DEFINITION genomic survey sequence.
ACCESSION CC607969
VERSION CC607969.1 GI:31969390
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 800)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OGUKR47V
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.

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Qy 361 GACATCAGTGCATCAACGGGGAGGTATGCGGGGGAGGTACAGCGGTGCTCTAGCT 420
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Qy 421 ACCTTGTCTTTAACTGCACACTGCACTCTGCACACTGCACACTAGTAGTAGTAGTCTAT 480
Db 367 -----CTGCACACTGCACACTAGTAGTAGTAGTCTAT 335
Qy 481 CTCTGCTGACCCAGCGCTTGTTCGTCGACAGTGGAGTTCCAGGTCGGCCCTGCGCTCGGC 540
Db 334 CTCTGCTGACCCAGCGCTTGTTCGTCGACAGTGGAGTTCCAGGTCGGCTCTGCGCTCGGC 275
Qy 541 GTCTCGGCGGGCGA-CAGCTTTGGGTGGCTCGCTACATTTTGAGGAAAAACGGTAGACCT 599
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Qy 600 GCGCCCTCGCGGTGTTCTGCTTCTTCG--CGAGACATGGCGTCTTTGGGCAAC 657
Db 214 CTAGACCTGCTGCGCGCATGCGCGGTGTTTCAGTTCTTCTTCTTCTTCTCGCCACAG 155
Qy 658 TTTCGCGGTGTCAGTGTGTTTTCGTCGATGAGACG--TGCTCTTTCCTGTCGATCGGAGA 714
Db 154 ATGCGGTGTCAGTGTGTTTTCGTCGATGAGACGTTTCTTCTTTCCTGTCGATCGGAGA 95
Qy 715 GGAT-ACCGAGATCCCGCGGTGGTGTCTTCTTCGACCCCAA--CCAATTGGGTGACCA 771
Db 94 GGATCACCAGATCGCGCGGTGGTGTCTCTCTCGACCCCAAGCAATTCGCGTGACCA 35
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Db 34 TTTCGCTACCAACAATTTTCGGTTTGGATATGTG 1
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LOCUS OGUKR47TH_ZM_0.7_1.5_KB_Zea_mays_genomic_clone_ZMMBMa0463G22,
DEFINITION genomic survey sequence.
ACCESSION CC607969
VERSION CC607969.1 GI:31969390
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 800)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OGUKR47V
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.

FEATURES
Location/Qualifiers
1..800
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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Db 547 AGTTTGGCCCTTCAAGTGGTTTCCCTCCAGCGGCTTTTCCACTTTGTGAAATG 606

Qy 1447 ACAACTGCACCACTTGTCTATTATATATATATAAAGGATAATATACTACAAAATATACA 1506

Db 607 ACAACTGCACCACTTGTCTATTATATATATATATACAGGATAATATACTACAAAATATATA 663

Qy 1507 ATACATCCATTCGATTTTATATTTTGTATCAATTTTCCCAAGTTTGTATCGACTCGCC 1566

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Qy 1624 TGCTAAATAATATACAGTAAATATAAATAATATAATTTTGTGAAATAAGACGAG 1683

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Qy 1684 CCAATTAATACTTGAATATAAAA 1707

Db 841 TCGATTAAACCTGAATATAATA 864

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LOCUS FURAA16TD_ZM_0.6_1.0_KB_Zea_mays_genomic_clone_ZM8Bta189C07, 974 bp DNA linear GSS 31-MAR-2003

DEFINITION genomic survey sequence.

ACCESSION CC013698.1 GI:29397202

VERSION

KEYWORDS

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE 1 (bases 1 to 974)

Whitehead, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,

Bennick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and

Bennetzen, J.

Maize Genomics Consortium

Unpublished (2003)

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TF

Class: sheared ends.

Location/Qualifiers

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CoT selected genomic DNA library"

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Best Local Similarity 86.9%; Pred. No. 2.8e-113;
Matches 668; Conservative 0; Mismatches 59; Indels 42; Gaps 5;

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Db 738 CCATGGTCGTACCTTCCCTCGCTGACGAAATGAACCGACCTTGTGGTACAGACATT 679

Qy 61 TCGTCGAAATGGTTCTTCTTACGCTGAGCCTGTGTAAATCCAGGTTCCGGATTGACGAG 120

Db 678 TCGTCGAAATGGTTCTTCTTACGCTGAGCCTGTGTAAATCCAGGTTCCGGATTGACGAG 619

Qy 121 AGTACACCTTCTCCAGAAGGACACCAAGTGGCTCTCGTTGGCCGCTGGCGGCTAC 180

Db 618 AGTACACCTTCTCCAGAAGGACACCAAGTGGCTCTCGTTGGCCGCTGGCGGCTAC 559

Qy 181 CTGCGCCTCAGTAGATTAGATGGATCTGCTGCCCTCCAGGCTCCAGCATATCCATGCG 240

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Qy 301 AAGTCTACGCGCGGACATCGTGGACCGCACTACAAGGCTGCTCTACGCGCGCATC 360

Db 438 AAGTCTACGCGCGGACATCGTGGACCGCACTACAAGGCTGCTCTACGCGCGCATC 379

Qy 361 GACATCAGTGCATCAACGGGAGGTCTATCGCGGAGGTACGCGGTGCTCTAGCT 420

Db 378 GACATCAGTGCATCAACGGGAGGTCTATCGCGGAGGTACGCGGTGCTCTAGCT 327

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Db 326 -----CTGCACACTGCACACTAGTAGTAGTAGTCTAT 294

Qy 481 CTCTGCTGACCCAGGCTTGTCTGGGACAGTGGGAGTTCCAGGTCGGCCCTGCGCTCGGC 540

Db 293 CTCTGCTGACCCAGGCTTGTCTGGGACAGTGGGAGTTCCAGGTCGGTCCTGCGCTCGGC 234

Qy 541 GTCTCGGCGCGGCA- CAGCTTGGGTGGGCTCGCTACATTCTTGAGGAAAACGCTAGACT 599

Db 233 GTCTCGGCGCGGCAAGCTCTGGGTGGCTCGCTACATTCTTGAGGTAGACGCTAGATCA 174

Qy 600 GCCCCTCGCGGCTGTGTCTCGGTTCTTCTCCG--CCGAGACATGGCGTGTCTTGGCAAC 657

Db 173 CTAGACCTGTCTGCCGATGCCGCTGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 114

Qy 658 TTGCGGTGTGAGT 714

Db 113 ATGGCGTGTGAGT 54

Qy 715 GGAT-ACCGAGATCGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 762

Db 53 GGATCACCAGATCGCGGCTGT 5

RESULT 7

CC937355

LOCUS

DEFINITION

CC937355

ACCESSION

CC937355

VERSION

KEYWORDS

SOURCE

ORGANISM

Zea mays

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 681)

Yu, Y., Kim, H.R., Hatfield, J., Soderlund, C., Bharti, A.K., Messing, J.

and Wing, R.

Sequencing of the maize genome

Unpublished (2003)

Contact: Rod Wing

Arizona Genomics Institute

University of Arizona

Biological Sciences West, 448A, P.O. Box 210089, Tucson, AZ

85721-0089, USA

[illegible]

Db	650	GTCTCGCCGCGCACCAGCTCTGGTGCGTCGCTACATCTTGTAGGTAGACGGTAGACCA	709
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Db	710	CTAGACTGTCTGCCGATGCGCGTGTTTCAGTTCATCTTCTTCTCCGCCGAC	769
Qy	657	CTTTGCCGTGTCACTGTGTTTTCGTATGAGAC	689
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Qy 657 CTTTCCGCTGCAGTGTTTTGTGATGAC 689
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Db 770 ATGGACGTGGTCAGTGTTTGTCTGATGAGAC 802

RESULT 10
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LOCUS	627 bp	DNA	linear	GSS 03-DEC-200
CG891370				

LOCUS	CG891370	827 bp	DNA	SSS 03-DEC-200
DEFINITION	ZMMBBB0371K12.r	ZMMBBB	Zea mays genomic clone	ZMMBBB0371K12.3'

genomic survey sequence.

CG891370

VERSION CG891370.1 GI:38645788

KEYWORDS GSS.

SOURCE	Zea mays
ORGANISM	Zea mays

ORGANISM Zea mays
Eukaryota. Viridiplantae. Streptophyta. Embryophyta. Tracheophyta.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
1 (bases 1 to 627)

AUTHORS Yu, Y., Kim, H.R., Hatfield, J., Soderlund, C., Bharti, A.K., Messing, J

and Wing, R.

TITLE	Sequencing of the maize genome
TOURNAY	published (2002)

JOURNAL
Unpublished (2003)
Contact: Rod Wing
COMMENT

COMMENT
CONTACT: ROD WING
Arizona Genomics Institute

**Arizona Genomics Institute
University of Arizona**

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ

85721-0088, USA

Tel: 520 626 3967

Fax: 520 621 9288

Email: <http://genome.arizona.edu>
ncp primers

PCR primers
FORWARD: T7

FORWARD: I /
BACKWARD: M13r

BACKWARD: MISS
plate: 0371 row: K column: 12

Seq primer: M13r

Class: BAC ends.

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Best Local Similarity 90.5%; Pred. No. 5.9e-96;
Matches 559; Conservative 0; Mismatches 38; Indels 21; Gaps 5;

Qy 841 CTGTGCATGCGTGTGACGTCGAGTCGCGTGTCCCGCGTCTGTTCTTGTGTGTCGAGATT 900
Db 29 CTCTTTAACGGGAAACTGCACTGCGTGTGTCGCGGTCTCTTGTGTGTCGCGA--- 85
Qy 901 CGTTCTCGGTGACACACACACACACCGCGCGAGCCAC--AAACGTGTAGCTCGCCCGGT 958
Db 86 -GTTCTCTCGGTGACACACACACACACCGCGCGAGCCACATATACGTGTAGCTCGCCCGGT 144
Qy 959 CGGAATCGGCAAGTGTCCAAAGCAAGCTTCAACGGATGCCGATGCTTCCGCGCGCGCG 1018
Db 145 CGGAATCGGCAAGT-----AGGCAAGCTTCAACGGATGCCGATGCTTCCGCGCGCGCG 199
Qy 1019 GGAGAGCTTGGCGGAGGACCTCGTCATCGGATCGGATCGGACGGTTGGATCGGAGAT 1078
Db 200 GGAGAGCTTGGCGGAGGACCTCGTCATCGGATCGGATCGGACGGTTGGATCGGAGAT 259
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Db 320 CATG-----ATTATTGTTGTAATTTGCAAAATTTCTGTATGTAATAATAATAATAAA 374
Qy 1199 TGAAGTAGTATCAGATGATCGGAGCTCGAAATACCGTAAGATGACCGGACGTCCGCG 1258
Db 375 TCAAGTAGTTTCAAGATGATCGGAGCTCGAAATACCGTAAGATGACCGGACGTCCGCG 434
Qy 1259 AGGTGCAGTCAGTTTAACTTTGAAATACCGTTAGCTTGGCTCGTTATTAGAGAGCT 1318
Db 435 AG-----GTGCAGTTGAGCTTGAATATACCGTTAGCTTGGCTCGTTATTAGAGAGCT 489
Qy 1319 CACGTAAACATATCTCTATCTCTACTACTATTGATTAATTAATTTCTACTATTAAATTA 1378
Db 490 CACGTATACAGATCTCTATCTCTACTACTATTGATTAATTAATTTCTACTATTAAATTA 549
Qy 1379 AATATACAGTTTCTCCCTTCATACATGTTTCCCTCTCCAGCGCGCTTTTCACCTGT 1438
Db 550 AATATACAGTTTCCGCTTCCCAAGTGTGTTTCTCTCCACGCGCGTTTTTCCCTTGG 609
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RESULT 11
LOCUS CG213069
DEFINITION CG213069 888 bp DNA linear GSS 22-AUG-2003
Ze mays genomic clone ZMMB0075A18,
genomic survey sequence.
ACCESSION CG213069
VERSION CG213069.1 GI:34112901
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 888)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
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Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OG3CJ09TV
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
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Best Local Similarity 84.2%; Pred. No. 7.1e-95;
Matches 631; Conservative 0; Mismatches 69; Indels 49; Gaps 8;

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Qy 248 AGCTGACGGAATGATCTGCGAGGACCTTACTACTCGCGCTCGGACGACGAAGTCCT 307
Db 121 AGCTGACGGAATGATCTGCGAGGACCTTACTACTCGCGCTCGGACGACGAAGTCCT 180
Qy 308 ACGGGCGGACATCGTGGAGCGCACATAAAGGCTCCCTCTACGCCGGATCGACATCA 367
Db 181 ACGGGCGGACATCGTGGAGCGGCACTAAGAGGCTGCTCTACGCCGGATCGACATCA 240
Qy 368 GTGGCATCAACGGGGAGGTTCATGCGGGGAGGTACAGCGTGTGCTCTAGTACCTTGT 427
Db 241 GTGGCATCAACGGGGAGGTTCATGCGGGGAGGTACAGCGTGTGCTCTAGTACCTTGT 285
Qy 428 CTTTAACTGCACACTGCACTCTGCACACTGCACAGCTAGTAGTATGCTATCTCTGCT 487
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Qy 488 GACCCAGGCTTGTTCGTGGAGAGTGGAGTTCACAGTTCGGCCCTCGCGCTCGCG 547
Db 326 GACCCAGGCTTGTTCGTGGAGAGTGGAGTTCACAGTTCGGCTCGCTCGCGCTCGCG 385
Qy 548 CCGGCGA-CAGCTTGGGTGGGCTCGCTACATTTCTTAGGAAACCGGTAGACCTGCCCT 606
Db 386 CCGGCGA-CAGCTTGGGTGGGCTCGCTACATTTCTTAGGAGTAGACGTAGACCACTAGACC 445
Qy 607 GCGGCTGTGTTGCTGCTTCTTCCG---CCGAGACATGGCGTGTTCCTTTCCTTTCCT 664
Db 446 TGTGCGGCATGCGCGCTGTGTTTCAGTCTTCTTCTTCTTTCCTTTCCTTTCCTTTCCT 505
Qy 665 TGTGAGTGTGTTTGTGCTGATGAGACG---TGTCTTCTTCTTCTTCTTCTTCTTCTTCTT 720
Db 506 GTTCAAGTGTGTTTGTGCTGATGAGACGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 565
Qy 721 CGAGATCGCGCGGTGTTGTTCTTCTTTCGACCCCAA--CCAATTCGGTGAACA--TTGCT 777
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Qy	468	AGTATGCTGCTATCTCTGCTGACCCAGGCTTGTCGTGGACAGTGGGGAGTTCACAGTCGG	527
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Qy	528	CCCTGCCGCTCGGCGTCTCGGCCCGCGCA - CAGCTTGGGGTGGGCTCGCTACATCTTTGAGGA	586
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432	TGTGACTGGCAGAGGATCACCGAGATCGCCGGCGTGTGTCTCTTCGACCCCAGGCCA	Db
759	AATTCCGGTGACCA-TTTCGGCTACCAACAATTTTGGGGTTTTGATGATGTGGGTCTCTGTATC	Qy
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[illegible]

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DEFINITION	OGVDX90TV ZM 0.7.1.5 KB zea mays genomic clone ZMMBMA0521012, genomic survey sequence.				
ACCESSION	CG303139				
VERSION	CG303139.1	GI:34217353			
KEYWORDS	GSS.				

SOURCE	ORGANISM
Zea mays	Zea mays
Zea mays	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
1 (bases 1 to 621)	Glomerata; Panicoidae; Andropogoneae; Zea.
REFERENCE	
AUTHORS	Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Numbarg, A., Robbins, D. and Lakey, N.
TITLE	Consortium for Maize Genomics

Unpublished (2002)
Other_GSSs: OGVDX90TH
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843
Fax: 301-838-0208
Email: white@tiger.org
Seq primer: TF

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Class: sheared ends.
FEATURES
  Location/Qualifiers
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Best Local Similarity 83.1%; Pred. No. 1.4e-76;
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206	Qy	TCTCGTGCTTCAGGCTTCAGGCCATATCGATGGCTTTTGATCGAGTCAAGCAATGATCCT	265
561	Db	TCCTGCTGCTTCAGGCTTCAGGCCATATCGAT--GCTTTTGATCGAGTCAAGCAATGATCCT	503
266	Qy	GGCAGGACCTTTACTCTGCGCCGTTCGGAGCGGAACAAGTCTACGGCGGGACATCGTGG	325
502	Db	GGCAGGACCTTTACTCTGCGCCGTTCGGAGCGGGAACAAGTCTACGGCGGGACATCGTGG	443
326	Qy	ACGGCGACTACAGGCTGCTCTACCGCGGCATCGACATCAGTGGCATCAACGGGAGG	385
442	Db	ACGGCGACTACAGGCTGCTCTCTACCGCGGCATCGACATCAGTGGCATCAACGGGAGG	383
386	Qy	TCATGCCGGGGCAGGTACAGCGTCTGCTCTAGCTACCTTGCTTTAACTGCACACTGCA	445
382	Db	TCATGCCGGGGCAGGTACAGCGTCTG-----	356
446	Qy	CTCTGCAACATGCAACAGTATAGTATGCTGCTATCTCTGTGTAACCAAGGCTTGTTCGTG	505
355	Db	--CTGCAACATGCAACAGTATAGTATGCTGCTATCTCTGTGTAACCAAGGCTTGTTCGTG	298
506	Qy	GACAGTGGGAGTTCCAGGTGGCCCTCGCGTGGCGCTCTGGCCGGCGGA--CAGCTTCGGT	564
297	Db	GACAGTGGGAGTTCCAGGTGGCTCTGCGCTGGCGCTCTGGCCGGCGGACACAGCTCTGGG	238
565	Qy	GGGCTCGCTACATTTCTTGAGAAACAGTATAGACCTGCCCCCTCGCGGCTGTGTTTCGGTTC	624
237	Db	TGGCTCGCTACATTTCTTGAGGTAGACGCTAGACCACTAGACCTGCTGCCGCAATCCGGCT	178
625	Qy	TTCTTTCG--CCGAGACATGGCGTCTTTGGCAACTTTTGGCGTGTCTAGTGTGTTTTCGTG	682
177	Db	GTGTTCAGTTCTTCTTTCTTCCTTCGCGCCAGACATGGCGTGTCTAGTGTGTTTTCGTG	118
683	Qy	ATGAGACG--TGTCCTTTTCCCTGTGACTGGCAGAGGAT--ACCGAGATCGCGCGCTGGT	738
117	Db	ATGAGACGTTTCTTCTTTCCCTGTGACTGGCAGAGGATCACCAGATCGCGCGCTGGT	58
739	Qy	TGTCCTTTCGACCCCAA--CCAAATTCGGTGAACA--TTGCGTACCAACAACATTTTGGG	792
57	Db	TGTCCTCTTCGACCCCAAGCAATTCGGGTGACATTTTCGTACCAACAACATTTTCGG	1

RESULT 14	BZ401579/c
LOCUS	BZ401579 TC ZM_0.7_1.5_KB Zea mays genomic clone ZMMBma0023A07,
DEFINITION	linear GSS 04-DEC-2002
ACCESSION	BZ401579
VERSION	BZ401579.1 GI:26026649
KEYWORDS	GSS.
SOURCE	Zea mays
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 737)
REFERENCE	Whitelaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T., Reinick,A., Fraser,C.M., Budiman,M.A., Beedell,J.A., Rohlfing,T., Citek,R.W., Numborg,A., Robbins,D. and Lakey,N. Consortium for Maize Genomics Unpublished (2002)
TITLE	Other_GSSs: OGABN93TM
JOURNAL	Contact: Cathy Whitelaw
COMMENT	TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843 Fax: 301-838-0208 Email: whitelaw@igr.org Seq primer: TF Class: sheared ends.

FEATURES	source	Location/Qualifiers
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ACCESSION	CG865571	
VERSION	CG865571.1	GI:38506429
KEYWORDS	GSS.	
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ORGANISM	Zea mays	
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REFERENCE	1 (bases 1 to 344)	
AUTHORS	Yu, Y., Kim H.R., Hatfield, J., Soderlund, C., Bharti, A.K., Messing, J.	
	and Wing, R.	

TITLE Sequencing of the maize genome
JOURNAL Unpublished (2003)
COMMENT Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: 17
BACKWARD: M13r
Plate: 0339 row: 0 column: 17
Seq primer: T7
Class: BAC ends.

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ORIGIN

Query Match 11.1%; Score 283.4; DB 9; Length 344;
Best Local Similarity 91.7%; Pred. NO. 3.6e-54;
Matches 311; Conservative 0; Mismatches 23; Indels 5; Gaps 1;
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Qy 1221 GACGTCGAAAATACCGTAAGAAATGACCGGACGTCGCGAGGTGCAGTTCAGTTAAACTT 1280
Db 61 GACGTCGAAAATACCGTAAGAAATGACCGGACGTCGCGAGGTGCAGTTCAGTTAAACTT 115
Qy 1281 GAAATACCGTTAGCGTTGGCCTCGTTATTAGAGAGCTCAGGTAACATATCTCTCTATC 1340
Db 116 GAAATACCGTTAGCGTTGGCCTCGTTATTAGAGAGCTCAGGTAACATATCTCTCTATC 175
Qy 1341 TCTACTACTATTGATTAATATCTTACTACTATTATTAAATATACAACTTCTCCCTTCA 1400
Db 176 TCTACTACTATTGATTAATATCTTACTACTATTATTAAATATACAACTTCTCCCTTCA 235
Qy 1401 TACATGGTTTCCCTCTCCAAGCGCGCTTTTCCACTTGTGAAAAATGACAACTGCACCACT 1460
Db 236 CAAGTGGTTTCCCTCTCCAAGCGCGCTTTTCCACTTGTGAAAAATGACAACTGCACCACT 295
Qy 1461 TGTCTATTATCTACTATATAAGGATAAATACTACAAAAA 1499
Db 296 TGTCTATTATCTACTATATAAGGATAAATACTACAAAAA 334

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 27, 2005, 14:02:42 ; Search time 416 Seconds
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Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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SUMMARIES

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2	79.2	3.1	1534	US-09-786-534-3	Sequence 3, Appli
3	74.4	2.9	2075	US-09-270-767-10495	Sequence 10495, A
C 4	68	2.7	601	US-09-949-016-70542	Sequence 70542, A
C 5	68	2.7	601	US-09-949-016-70543	Sequence 70543, A
6	68	2.7	2226	US-09-799-451-355	Sequence 355, App
7	68	2.7	2727	US-09-814-915A-36	Sequence 36, Appl
8	68	2.7	2813	US-09-949-016-2085	Sequence 2085, Ap
9	68	2.7	12981	US-09-949-016-13827	Sequence 13827, A
10	66.6	2.6	187169	US-09-949-016-12776	Sequence 12776, A
11	66.6	2.6	191569	US-09-949-016-15940	Sequence 15940, A
12	66.4	2.6	13254	US-08-276-852-156	Sequence 156, App
C 13	66.4	2.6	13254	US-08-276-852-170	Sequence 170, App
C 14	66.4	2.6	13254	US-08-899-575-156	Sequence 156, App
C 15	66.4	2.6	13254	US-08-899-575-170	Sequence 170, App
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C 19	66.4	2.6	13254	PCT-US95-08743-170	Sequence 170, App
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C 21	66.4	2.6	105919	US-09-949-016-11769	Sequence 11769, A
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C 25	65.2	2.6	601	US-09-949-016-37151	Sequence 37151, A
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C 32	65.2	2.6	601	4	US-09-949-016-146137	Sequence 146137,
C 33	65.2	2.6	601	4	US-09-949-016-146404	Sequence 146404,
C 34	65.2	2.6	601	4	US-09-949-016-146405	Sequence 146405,
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39	65.2	2.6	223471	4	US-09-949-016-12724	Sequence 12724, A
C 40	63.8	2.5	18773	4	US-09-949-016-12725	Sequence 12725, A
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C 43	63.2	2.5	601	4	US-09-949-016-168054	Sequence 168054,
C 44	63.2	2.5	601	4	US-09-949-016-168055	Sequence 168055,
C 45	63.2	2.5	601	4	US-09-949-016-168056	Sequence 168056,

ALIGNMENTS

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US-09-786-534-1
; Sequence 1, Application US/09786534
; Patent No. 6727095
; GENERAL INFORMATION:
; APPLICANT: Tischner, Rudolf
; APPLICANT: Hoffmann, Guido
; TITLE OF INVENTION: GENETICALLY MODIFIED SUGARBET
; FILE REFERENCE: P/2107-170
; CURRENT APPLICATION NUMBER: US/09786.534
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: PCT/EP99/06522
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 198 40 964.8
; PRIOR FILING DATE: 1998-09-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1068
; TYPE: DNA
; ORGANISM: Beta vulgaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1068)
US-09-786-534-1

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Qy	328	CGCAGCTACAGGCTGCTCTACGCGGACATCACATCAGTGGCATCAACGGGAGGTC	387	
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; Sequence 3, Application US/09786534
; Patent No. 6727095
; GENERAL INFORMATION:
; APPLICANT: Tischner, Rudolf
; APPLICANT: Hoffmann, Guido

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; TITLE OF INVENTION: GENETICALLY MODIFIED SUGARBEEF
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; FILE REFERENCE: P/2107-170
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; PRIOR FILING DATE: 1998-09-08
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; SOFTWARE: PatentIn Ver. 2.0
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; LENGTH: 1534
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RESULT 3
US-09-270-767-10495
; Sequence 10495, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10495
; LENGTH: 2075
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-10495

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[illegible]

RESULT 4
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; Sequence 70542, Application US/09949016
; Patent NO. 6812339
; GENERAL INFORMATION:

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? APPLICANT: VENTER, J. Craig et al.
? TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
? TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
? FILE REFERENCE: CL001307
? CURRENT APPLICATION NUMBER: US/09/949,016
? CURRENT FILING DATE: 2000-04-14
? PRIOR APPLICATION NUMBER: 60/241,755
? PRIOR FILING DATE: 2000-10-20
? PRIOR APPLICATION NUMBER: 60/237,768
? PRIOR FILING DATE: 2000-10-03
? PRIOR APPLICATION NUMBER: 60/231,498
? PRIOR FILING DATE: 2000-09-08
? NUMBER OF SEQ ID NOS: 207012
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 70542
? LENGTH: 601
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? US-09-949-016-70542

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Qy	331	CACCTACAAGGCCCTGCTCTTACGGCGGCATCGACATCATAGTGCATCAACGGGAGGTCATG	390		
Db	218	CATTACGGGCGCTGCTGTATGTGAGTCAAGATTCCGGGGACTATGCCGAGGTCATG	159		
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US-09-949-016-70543/c
Sequence 70543, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 70543
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TYPE: DNA
ORGANISM: Human
US-09-949-016-70543

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				Gaps	0;
Qy	271	GGACCTTACTACTGCGCCGTGGAGCGGA	CAAGTCTTACGCGGCGGGA	CATGTCGACGCG	330
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Qy	331	CACCTACAAGCGCCTGCCTCTACGCGGGCAT	CGACATCATAGTGGCATCAACGCGGAGGTCATG		390
Db	414	CATTACCGGCGCTTGTGTATGCTGGAGTCAAG	ANTTCCGGGGACTAATGCCAGGTCATG		355

Qy 391 CCGGGCAGGTA 402
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Db 354 CCGCCAGGTA 343

RESULT 6

US-09-799-451-355
; Sequence 355, Application US/09799451
; Patent No. 6783969

GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yunqing
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.

; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides

; FILE REFERENCE: 803

; CURRENT APPLICATION NUMBER: US/09/799,451

; CURRENT FILING DATE: 2001-03-05

; NUMBER OF SEQ ID NOS: 948

; SOFTWARE: pt_FL_genes Version 2.0

; SEQ ID NO 355

; LENGTH: 2226

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (211)..(1212)

US-09-799-451-355

Query Match 2.7%; Score 68; DB 4; Length 2226;

Best Local Similarity 69.7%; Pred. No. 1.2e-07;

Matches 92; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

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Db 598 CAGGTCCATATTACTGTGGTGGAGCAGACAGAGCCTATGGCAGGACATCGTGGAG 657

Qy 328 GCGCACTACAAGCGCTGCTTACCGCGGCATCGACATCAGTGGCATCAACGGGGAGGTC 387
|||
Db 658 GCCATTACCGGCGCTGCTTGTATGCTGGAGTCAAGATTGCGGGGACTAATGCCGAGGTC 717

Qy 388 ATGCCGGGGCAG 399
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Db 718 ATGCTGCCCGAG 729

RESULT 7

US-09-814-915A-36

; Sequence 36, Application US/09814915A

; Patent No. 6750015

GENERAL INFORMATION:

; APPLICANT: Horwitz, Kathryn

; APPLICANT: Richer, Jennifer

; TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methods Relat

; TITLE OF INVENTION: Thereto

; FILE REFERENCE: 2848-39

; CURRENT APPLICATION NUMBER: US/09/814,915A

; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: 60/214,870
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 36

; LENGTH: 2727

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-814-915A-36

Query Match 2.7%; Score 68; DB 4; Length 2727;

Best Local Similarity 69.7%; Pred. No. 1.3e-07;

Matches 92; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

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Db 581 CAGGTCCATATTACTGTGGTGGAGCAGACAGAGCCTATGGCAGGACATCGTGGAG 640

Qy 328 GCGCACTACAAGCGCTGCTTACCGCGGCATCGACATCAGTGGCATCAACGGGGAGGTC 387
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Db 641 GCCATTACCGGCGCTGCTTGTATGCTGGAGTCAAGATTGCGGGGACTAATGCCGAGGTC 700

Qy 388 ATGCCGGGGCAG 399
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Db 701 ATGCTGCCCGAG 712

RESULT 8

US-09-949-016-2085

; Sequence 2085, Application US/09949016

; Patent No. 6812339

GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2085

; LENGTH: 2813

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-2085

Query Match 2.7%; Score 68; DB 4; Length 2813;

Best Local Similarity 69.7%; Pred. No. 1.4e-07;

Matches 92; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

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Qy 328 GCGCACTACAAGCGCTGCTTACCGCGGCATCGACATCAGTGGCATCAACGGGGAGGTC 387
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Db 618 GCCATTACCGGCGCTGCTTGTATGCTGGAGTCAAGATTGCGGGGACTAATGCCGAGGTC 677

Qy 388 ATGCCGGGGCAG 399
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Db 678 ATGCTGCCCGAG 689

RESULT 9

US-09-949-016-13827

; Sequence 13827, Application US/09949016

Db 8959 ATGCCCTGCCGAG 8970

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RESULT 13
US-08-276-852-170/c
: Sequence 170. Application US/08276852

GENERAL INFORMATION:
 APPLICANT: Burton, Dennis R
 APPLICANT: Barbas, Carlos F
 APPLICANT: Lerner, Richard A
 TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 NUMBER OF SEQUENCES: 170
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: The Scripps Research Institute, Office of
 ADDRESSEE: Patent Counsel
 STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
 STREET: Mail Drop TPC8
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRL452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 170:
SEQUENCE CHARACTERISTICS:
LENGTH: 13254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
US-08-276-852-170

Query Match      2.6%; Score 66.4; DB 1; Length 13254;
Best Local Similarity 68.9%; Pred. No. 9.3e-07;
Matches 91; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

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[illegible]

US-08-899-575-156

; Sequence 156, Application US/08899575
; Patent No. 5770440

; GENERAL INFORMATION:

; APPLICANT: Burton, Dennis R

; APPLICANT: Barbas, Carlos F

; APPLICANT: Lerner, Richard A

; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS

; NUMBER OF SEQUENCES: 170

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: The Scripps Research Institute, Office of

; ADDRESSEE: Patent Counsel

; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,

; STREET: Mail Drop TPC8

; CITY: La Jolla

; STATE: CA

; COUNTRY: USA

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/899,575

; FILING DATE: 24-JUL-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/276,852

; FILING DATE: 18-JUL-1994

; APPLICATION NUMBER: US 08/178,302

; FILING DATE: 30-SEP-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/954,148

; FILING DATE: 30-SEP-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Fitting, Thomas

; REGISTRATION NUMBER: 34,163

; REFERENCE/DOCKET NUMBER: SCR1452P

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619-554-2937

; TELEFAX: 619-554-6312

; INFORMATION FOR SEQ ID NO: 156:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 13254 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: circular

; MOLECULE TYPE: DNA (genomic)

; US-08-899-575-156

Query Match 2.6%; Score 66.4; DB 1; Length 13254;

Best Local Similarity 68.9%; Pred. No. 9.3e-07;

Matches 91; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 268 CAGGACCTTACTACTCGCGCTCGGACGCGACAAGTCTCTACGCGCGGACATCGTGGAC 327

Db 8839 CAAGGTCCGTATTACTGTGTGGCGCAGACAAAGCCTATGGCAGGGATATCGTGAG 8898

Qy 328 GCGCACTACAGGCTCTCTACGCGGCATCGACATCAGTGGCATCAACGGGGAGTTC 387

Db 8899 GCTCACTACCGCGCTCTGTGTATGCTGGGCTCAAGATTACAGGAACAAATGCTGAGTTC 8958

Qy 388 ATGCCGGGGCAG 399

Db 8959 ATGCTGCCCCAG 8970

RESULT 15

US-08-899-575-170/c

; Sequence 170, Application US/08899575

; Patent No. 5770440

; GENERAL INFORMATION:

; APPLICANT: Burton, Dennis R

; APPLICANT: Barbas, Carlos F

; APPLICANT: Lerner, Richard A

; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS

; NUMBER OF SEQUENCES: 170

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: The Scripps Research Institute, Office of

; ADDRESSEE: Patent Counsel

; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,

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; COMPUTER READABLE FORM:

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; COMPUTER: IBM PC compatible

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; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/899,575

; FILING DATE: 24-JUL-1997

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; PRIOR APPLICATION DATA:

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; ATTORNEY/AGENT INFORMATION:

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Query Match 2.6%; Score 66.4; DB 1; Length 13254;

Best Local Similarity 68.9%; Pred. No. 9.3e-07;

Matches 91; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 268 CAGGACCTTACTACTCGCGCTCGGACGCGACAAGTCTCTACGCGCGGACATCGTGGAC 327

Db 4416 CAAGTCCGTATTACTGTGTGGCGCAGACAAAGCCTATGGCAGGGATATCGTGAG 4357

Qy 328 GCGCACTACAGGCTCTCTACGCGGCATCGACATCAGTGGCATCAACGGGGAGTTC 387

Db 4356 GCTCACTACCGCGCTCTGTGTATGCTGGGCTCAAGATTACAGGAACAAATGCTGAGTTC 4297

Qy 388 ATGCCGGGGCAG 399

Db 4296 ATGCCTGCCAG 4285

Search completed: April 27, 2005, 20:23:43

Job time : 419 secs